

178655

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Monday, February 06, 2006 10:21 AM
To: Yu, Misook; STIC-Biotech/ChemLib
Subject: RE: rsuh search request 10/111,257

~~Please rush. Thanks Chris~~

CRIF

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Yu, Misook
Sent: Monday, February 06, 2006 9:09 AM
To: Chan, Christina
Subject: rsuh search request 10/111,257

Pls approve rush search for the case due this biweek.

Stic, pls search SEQ ID NO: 3 (nucleic acid).

Examiner Misook Yu, Ph.D.
571-272-0839 (phone)
571-273-0839 (fax)
Art Unit 1642
REM-3D29 (Office)
REM-3C18 (Mail Box)
400 Dulany Street
Alexandria, VA 22314

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 6, 2006, 16:26:26 ; Search time 8168 Seconds
(without alignments)

11542.112 Million cell updates/sec

Title: US-10-111-257-3

Perfect score: 2015

Sequence: 1 cgcctcgcacacggtgacgc.....gtgaagttctcaactaaa 2015

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_hic.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_est7.*

9: gb_gss1.*

10: gb_gss2.*

11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1964.2	97.5	5165	4	CR749560 Homo sapi
2	1845.6	91.6	3850	4	CR857633 Pongo pyg
3	1383	68.6	1383	11	DO045794 Homo sapi
4	867	43.0	935	5	BU944114 AGENCOURT
5	802.2	39.8	839	3	BM014339 603640139
6	748	37.1	909	7	CT001323 CT001323
7	738.4	36.6	915	5	BU176917 AGENCOURT
8	730.6	36.3	940	5	BU539183 AGENCOURT
9	718.2	35.6	756	1	AM736896 IL3-CT021
10	711.6	35.3	890	5	BO719354 AGENCOURT
11	707	35.1	731	8	CR869347 HESG4_34
12	666	33.1	692	7	CN389062 170004240
13	664	33.0	696	7	CN389072 170004240
14	663.2	32.9	709	11	DO045795 Pan trogl
15	648.2	32.2	656	7	CK003957 AGENCOURT
16	647.4	32.1	684	7	CN389071 170006000
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18	618.6	30.7	1755	11	DO050311 Homo sapi
19	611	30.3	680	2	BE742835 601574472
20	604.8	30.0	873	5	BF685522 602142247
21	604.8	30.0	873	5	BU150858 AGENCOURT
22	592.4	29.4	715	1	AM601306 PMO-BT034

23	587.8	29.2	658	2	BF001707 792a12.x
24	582.2	28.9	601	1	AM367440 MRO-HT016
25	581.8	28.9	840	5	BU176890 AGENCOURT
26	570	28.3	3261	4	CR860800 Pongo pyg
27	567	28.1	582	3	BP293039 BP293039
28	566.6	28.1	697	6	CD641275 AGENCOURT
29	564.4	28.0	2919	4	BC040591 Homo sapi
30	562.8	27.9	2299	4	AF161544 Homo sapi
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32	558.2	27.7	617	8	W72665
33	553	27.4	702	1	AG142996 Pan trogl
34	546.6	27.1	594	2	BE178353 RC3-HT060
35	546	27.1	1467	11	DO032599 Homo sapi
36	543.8	27.0	616	2	BE178002 RC3-HT060
37	541.6	26.9	744	10	AG143038 Pan trogl
38	538.4	26.7	744	6	CD521516 AGENCOURT
39	538	26.7	1929	11	DO045890 Homo sapi
40	534.2	26.5	548	9	AO580696 RPI-11-4
41	534.2	26.5	679	2	BG718400 602696429
42	531.4	26.4	755	6	CD520335 AGENCOURT
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44	529	26.3	582	3	BP361237 BP361237
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ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

KEYWORDS

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

CONSRM

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 5165
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ORIGIN

Query Match	97.5%;	Score 1964.2;	DB 4;	Length 5165;
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OY	47	TAGGCAAGCATCTCTTACAAAAAGCATCCCGAGGAGGAAGACGAATCGTTAAACATCTT	106
Db	1205	CAGGCGACGATCTTTCAGAAAAAGCATCCCGAGGAGGAAGACGAATCGTTAAACATCTT	1264
OY	107	AGGTCAGCTCAGCCTCTCGAATTGCTCTTTCAGTGAAGAACCCGAGAACTGATC	166
Db	1265	AGGTCAGCTCAGCCTCTCGAATTGCTCTTTCAGTGAAGAACCCGAGAACTGATC	1324
OY	167	AGTTCCTCAGTTCTAACAATGGCCCAAGGTTTGTAAGTTGCGCCGACGTAGCATAG	226
Db	1325	AGTTCCTCAGTTCTAACAATGGCCCAAGGTTTGTAAGTTGCGCCGACGTAGCATAG	1384
OY	227	ACTTTTCTCAGAGGAGTGGGCGTGTCTGAAGCTCGCTCAGAGGGAAGCTGTGATCGGGAG	286
Db	1385	ACTTTTCTCAGAGGAGTGGGCGTGTCTGAAGCTCGCTCAGAGGGAAGCTGTGATCGGGAG	1444
OY	287	TGATGCTGAGAACTACAGTAATTGATCTCACTGATTTGGAGTCAGCATATGAAATA	346
Db	1445	TGATGCTGAGAACTACAGTAATTGATCTCACTGATTTGGAGTCAGCATATGAAATA	1504
OY	347	AGAGTTTACCTACAGAAAAAAACATTCTGAATAGGAGCTTCCAAAAGAAATTCAGATA	406
Db	1505	AGAGTTTACCTACAGAAAAAAACATTCTGAATAGGAGCTTCCAAAAGAAATTCAGATA	1564
OY	407	GAAGAAGTAATCCCTTGCGCGTAATCTGSAATGTGAAGGTAACGCTTGAAAGACACAGC	466
Db	1565	GAAGAAGTAATCCCTTGCGCGTAATCTGSAATGTGAAGGTAACGCTTGAAAGACACAGC	1624
OY	467	GCTCAGAGGGAGGTATGCATTCAGATGATCATGAATTAATGTCAAAAGGCGTGCTACTA	526
Db	1625	GCTCAGAGGGAGGTATGCATTCAGATGATCATGAATTAATGTCAAAAGGCGTGCTACTA	1684
OY	527	GAGAAGGACCCCTCTAGAACACATCAGAGACATCATPAGAGAAATTCCTTGTGATGTA	586
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OY	587	AGGACTGTGGGAAGGCTTTTAGTGTGTGCTATCAACTTAGCAATCAGAAAATCCATA	646
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OY	707	TTACTCAACATCAAAAAATTCATACCTGGGGAAGAGCCCTACGAATGTAAAGACTGTGGGA	766
Db	1865	TTACTCAACATCAAAAAATTCATACCTGGGGAAGAGCCCTACGAATGTAAAGACTGTGGGA	1924
OY	767	AGGCTTTTTCGATGGGAGCTCAAGCCTCGTATTCATPAGAGATTCAATCTGTGTGAAGAAC	826
Db	1925	AGGCTTTTTCGATGGGAGCTCAAGCCTCGTATTCATPAGAGATTCAATCTGTGTGAAGAAC	1984
OY	827	CCTATGATGTAAGACTGTGGAAGAGCCTTTTCGGGTGTGATGAGCTCACTCAGACACC	886

Db	1985	CCTATGATGTAAAGACTGTGGAAAGGCGCTTTGGCGGTGTGANTGACCTCAGCAGACC	2044
Qy	887	AGAGATTCACACTGTGGGAGAAAGACTACGATGCAAAAGACTGTGGAGACCTTTAGCC	946
Db	2045	AGAGATTCACACTGTGGGAGAAAGACTACGATGCAAAAGACTGTGGAGACCTTTAGCC	2104
Qy	947	GTGTGTATTAACCTTATTCAGACCAAGAAATTCATATGTGGGAGAAAGCTTTACGAGTGA	1006
Db	2105	GTGTGTATTAACCTTATTCAGACCAAGAAATTCATATGTGGGAGAAAGCTTTACGAGTGA	2164
Qy	1007	AAGACTGTGGAGAGGCTTTTATTTGTGTGTTCAAGCCTCATTTCAAGCATTAAGAAATTCACA	1066
Db	2165	AAGACTGTGGAGAGGCTTTTATTTGTGTGTTCAAGCCTCATTTCAAGCATTAAGAAATTCACA	2224
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Db	2225	CAGGTGAGAAACCTTATGATGTGCAGAATGTGGAAAGGCTTTATCTCGAGTCAATTACC	2284
Qy	1127	TTACTCGACATCAAAAGATCCACACGGGTGGAAGGCTCACGAATGTAAAGAGTGTGGGA	1186
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Qy	1187	AGGCTTTTCGTGGGGTTCGAGCCTCGTTAAGCAGAGAGATTCATACGGGCGAGAAGC	1246
Db	2345	AGGCTTTTCGTGGGGTTCGAGCCTCGTTAAGCAGAGAGATTCATACGGGCGAGAAGC	2404
Qy	1247	CGTACAGTGCACAGATGTGGGAAGGCTTCAATTGTGCTATCACTCACTACAGACG	1306
Db	2405	CGTACAGATGCACAGAGTGTGGGAAGGCTTCAATTGTGCTATCACTCACTACAGACG	2464
Qy	1307	AGAGAAATCCACACAGGGGAAACCCCGTAAATGTAAAGAGTGTGGGAAGGCTTCAATT	1366
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Qy	1487	GTGGGGCGAAATCTTACGAAATGTAAAGAGTGTGGGAAGGCTGTAAACCACTTAACCATC	1546
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Qy	1547	TCCGGAACATCAGAGATTCACAAACAGTTGAAGAGCTTTTGAACGAGTAGCCCGCTC	1606
Db	2705	TCCGGAACATCAGAGATTCACAAACAGTTGAAGAGCTTTTGAACGAGTAGCCCGCTC	2766
Qy	1607	GTATCTATGTTCGCTTTCACAGTTTGTATCTGACGTCAACTGCAGTTCAAAAAATAT	1666
Db	2765	GTATCTATGTTCGCTTTCACAGTTTGTATCTGACGTCAACTGCAGTTCAAAAAATAT	2824
Qy	1667	TAAATGMAAATTCAGAAATTAAGAAATTTTAAGTCTCAAAATGTGTGCCCTTCTGAGTA	1726
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Qy	1787	TCCAGCACATCCACGCTGTATACGCCACCAACCTGCTAAGTACCTTAAGACCGTCTTGG	1846
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Qy	1847	TGATCAGATCAACTATCCACAGATCACAGTGTCTGTGCCCAATGATCTCACTTGTCTT	1906
Db	3005	TGATCAGATCAACTATCCACAGATCACAGTGTCTGTGCCCAAGCAGTCTCTCACTTGTCTT	3064
Qy	1907	AACAGTGGCCCCAGAGACAGAGATGATGATGTGTGTATTCGATATGCCAATAGAGAAG	1966
Db	3065	AACAGTGGCCCCAGAGACAGAGATGATGATGTGTGTATTCGATATGCCAATAGAGAAG	3124

QY 1967 CCACAAGTCTCTCTTTAAATGAAGTGAAGTCTCAACTTAA 2015
DB 3125 CCACAAGTCTCTCTTTAAATGAAGTGAAGTCTCAACTTAA 3173

RESULT 2
CR857633

LOCUS CR857633 3850 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA, cDNA DKFp459H0254 (from clone DKFp459H0254).
ACCESSION CR857633
VERSION CR857633.1 GI:55726270
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo.
1 (bases 1 to 3850)
Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amid, C., Oeanger, A.,
Fodor, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY

COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA
Sequencing consortium of the German Genome Project. This clone
(DKFp459H0254) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFp459H0254
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
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/note="zinc finger protein 331 (Homo sapiens)"
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ORIGIN
Query Match 91.6%; Score 1845.6; DB 4; Length 3850;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1905; Conservative 0; Mismatches 39; Indels 6; Gaps 3;

QY 72 ATCCCGAGAGAGAGAGAGATCGTTAAACATCTTA--GTCAGCTCAGCCTCTCGA 128
DB 1 ATCCCGAGAGAGAGAGAGATCGTTAAACATCTTAAGGTCAGCTCAGCCTCTCGA 60

QY 129 ATT--TGNCTTTCAGTGAAGAAACCCGAGAAAGTGAATGATTCAGTCTTAACA 186
DB 61 ATTGTGCTCTTCAAGTGAAGAAACCCGAGAAAGTGAATGATTCAGTCTTAACA 120

QY 187 ATGGCCAGAGGTTTGTGACGTTCCCGACGTAAGCCATGACTTTCTCAGAGAGATGG 246
DB 121 ATGGCCAGAGGTTTGTGACATTCGCGCATGTAGACATAGACTTTCTCAGAGAGATGG 180

QY 247 GCTGTCTGAACCTGTCTCAAGGAGGACTGTACCTGGACGTGATCTGTGAGAACTACGT 306
DB 181 GCTGTCTGAACCTGTCTCAAGGAGGACTGTACCTGGACGTGATCTGTGAGAACTACGT 240

QY 307 AACTGTGCTCAGCGAATTTGGAGTCAACATATGAAATTAAGATTACCTACAGAAAA 366
DB 241 AACTGTGCTCAGCGAATTTGGAGTCAACATATGAAATTAAGATTACCTACAGAAAA 300

QY 367 AACATTCAATGAATTAAGAGGCTTCCAAAAGAAATTCAGATAGAAAGTAATCCCTTGGC 426
DB 301 AACATTCAATGAATTAAGAGGCTTCCAAAAGAAATTCAGATAGAAAGTAATCCCTTGGC 360

QY 427 CGTAACTGAATATGTGAAGGTAAGCTTGAAGAACCAAGCGCTCCAGAGGAGATGTTC 486
DB 361 CGTAACTGAATATGTGAAGGTAAGCTTGAAGAACCAAGCGCTCCAGAGGAGATGTTC 420

QY 487 AATCAGATGATCATCAATTAATGTCAAAAGCGCTGCTACTAGAGAGGACCCCTCTGA 546
DB 421 AATCAGATGATCATCAATTAATGTCAAAAGCGCTGCTACTAGAGAGGACCCCTCTGA 480

QY 547 ACACATCAGAGACATCATTAAGAGAAATTCCTTGAATGTGAAGACTGTGGAGAGGCTTT 606
DB 481 ACACATCAGAGACATCATTAAGAGAAATTCCTTGAATGTGAAGACTGTGGAGAGGCTTT 540

QY 607 AGCTGTGCTATCAACTTAAGTCAACATCAAGAAATTCATCTGTGAGAGAACTTATGA 666
DB 541 AGCTGTGCTATCAACTTAAGTCAACATCAAGAAATTCATCTGTGAGAGAACTTATGA 600

QY 667 TGTAAAGATGTAAAGAGGCTTCCGTTGGGCAATTCAGCTTCAACATCAAAAAATT 726
DB 601 TGTAAAGATGTAAAGAGGCTTCCGTTGGGCAATTCAGCTTCAACATCAAAAAATT 660

QY 727 CATATCGGGAGAGAGCCCTTACGATGTAAAGACTGTGGAGAGGCTTTGATGGGGCTCA 786
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QY 787 AGCTGTGATTCATTAAGAGATTCATCTGTGAAAAACCTATGAATGTAAAGACTGT 846
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QY 907 AAAGACTACGAATGCAAGAACTGTGGAGAACTTTAGCCGTGTATTAACCTTATTGAG 966
DB 841 AAAGACTACGAATGCAAGAACTGTGGAGAACTTTAGCCGTGTATTAACCTTATTGAG 900

QY 967 CACAAGAGATTCATTAAGTGGGAGAGGCTTACGAGTGTAAAGACTGTGGAGAGGCTTTT 1026
DB 901 CACAAGAGATTCATTAAGTGGGAGAGGCTTACGAGTGTAAAGACTGTGGAGAGGCTTTT 960

QY 1027 ATTTGTGTTCAAGGCTTCAATTCAGATTAAGAAATTCACAGGTGTGAAGAAACCTATGAA 1086
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QY 1207 AGCTCGTTAAGCAGAGATACATACGAGGAGAACCGCTACAGTGCACAGATGT 1266
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QY 1327 ACCCGCTAATAATGTAAAGAGTGTGGAAAGCGCTTCAATTATGATGAGAGCGCTCGGAA 1386
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DB 1381 AGTCATGGCCATCAGCTTACACAAATCAGAAACGCAAGTGGGCGAAATCTTACGAA 1440
QY 1507 TGTAAAGAGTGGGAGGAGCATGTACCACTTAAACATCTCCGAGAACATCAGAGATC 1566
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QY 1567 CACAAAGTTGAAGAGCCTTTTGAACGAGTAGCCGCTGTATCTATGATGTTGCTTTC 1626
DB 1501 CACAAAGTTGAAGAGCCTTTTGAACGAGTAGCCGCTGTATCTATGATGTTGCTTTC 1560
QY 1627 CACAGTTTGTATCTGCACTCAATCAGAGTTCAAAATATTAATGAAATTCAGAA 1686
DB 1561 CACAGTTTGTATCTGCACTCAATCAGAGTTCAAAATATTAATGAAATTCAGAA 1620
QY 1687 TAAAGAAATT-TAAGTCTAAATGATGTCCTTCTGAGAGGAGTGAATCTCTCG 1745
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QY 1746 TGTCCGCTCAGCCGCGCGGAGTGAATCATCCCTTGTCCAGACATCCAGCTGT 1805
DB 1681 TGTCCGCTCAGCCGCGCGGAGTGAATCATCCCTTGTCCAGACATCCAGCTGT 1740
QY 1806 ATACGCCACCCACCTGCTATGATGATTAAGCGCTTGTGTATGATCAATCAATCCC 1865
DB 1741 ACACGCTACCCACCTGCTATGATGATTAAGCGCTTGTGTATGATCAATCAAT 1800
QY 1866 AGATATCAGTGTCTGTGCTCAAGTGTCTCACTTGTCTTACAGTGTCCAGAGAGC 1925
DB 1801 AGATATCAGTGTCTGTGCTCAAGTGTCTTCTTGTCTTACAGTGTCCAGAGAGC 1860
QY 1926 AGAGATGATGATGCTGTGATTCGATATGCCAAAGAGAGCCAAAGTCTTCTTTT 1985
DB 1861 AGAGATGATGATGCTGTGATTCGATATGCCAAAGAGAGCCAAAGTCTTCTTTT 1920
QY 1986 AATGAAAAGGTGAAGTTCTCACTTAA 2015
DB 1921 AATGAAAAGGTGAAGTTCTCACTTAA 1950

RESULT 3
LOCUS DQ045794 1383 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens ZNF463 gene, VIRIDAL TRANSCRIPT, partial sequence,
ACCESSION DQ045794
VERSION DQ045794.1 GI:66897009
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1383)
Nietzen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,

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TITLE
JOURNAL
PUBMED
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JOURNAL
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AACTGTCTCAAGAGGACCTGTATCTGGAGCGTGAATGCTGGAGAAATCAATGTAATCTTGTCTG 120
QY 316 TCACGTGATTTGAGTGCAGCATATGAAATTAAGATTTACTTACAGAAAAAATTCAT 375
DB 121 TCACGTGATTTGAGTGCAGCATATGAAATTAAGATTTACTTACAGAAAAAATTCAT 180
QY 376 GAAATTAAGGCTTCCAAAAGAAATTCAGATAGAGAAATTCCTTGGCGGTAACTGG 435
DB 181 GAAATTAAGGCTTCCAAAAGAAATTCAGATAGAGAAATTCCTTGGCGGTAACTGG 240
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DB 241 ATATGTGAAGGTATCGCTTAAAGACCAAGCGCTCCAGAGGAGATATCAATCAAGATG 300
QY 496 ATCATCAATTAATGTCAAAAAGGCTGTCTACTAGAGAGGACCCCTCTAGAACATCAAG 555
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QY 556 AGACATCATAGAGAGATTCCTTTGATGTAAAGACTGTGGAAAGCGCTTTAGTGTGTGC 615
DB 361 AGACATCATAGAGAGATTCCTTTGATGTAAAGACTGTGGAAAGCGCTTTAGTGTGTGC 420
QY 616 TATCAACTTATGTCAACATCAAGAAATCCATATCTGTGAGAAAACTTATGAATGTAAGAA 675
DB 421 TATCAACTTATGTCAACATCAAGAAATCCATATCTGTGAGAAAACTTATGAATGTAAGAA 480
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DB 541 GAGAAAGCCTTCAAGATGTAAGAATCTGTGGAAAGCGCTTTTCAATGGGCTCAAGCTCGTT 600
QY 796 ATTCAATTAAGAGATTTATATCTGTGTAAGAAACCTTATGAATGTAAAGACTGTGAAAGGCC 855
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QY 916 GAATGCAAGAGCTGTGGGAGAGCTTTAGCCGTGTATTAACCTTATTGACAGCAAGAGA 975
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Db 1381 TGA 1383

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RESULT 4
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DEFINITION AGENCOURT 10544811 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6728338 5', mRNA sequence.
ACCESSION BU944114
VERSION BU944114.1 GI:24132933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 935)
REFERENCE NIH-MGC http://mgi.mgi.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov

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Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
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 High quality sequence stop: 669.
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 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library."

ORIGIN

Query Match 43.0%; Score 867; DB 5; Length 935;
 Best Local Similarity 99.0%; Pred. No. 5; 6e-236;
 Matches 903; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

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QY 307 AACTGTGCTCACTGATTTGGAAGTCAAGATGAAATTAAGATTACTCAGAGAGAA 366
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QY 367 AACATTCAAGAAATTAAGGCTTCCAAAAGAAATTCAGATGAAGAAATTCCTTGGC 426
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Db 661 GGAAGAGGCGCTTTCCGGGTGTGATGAGCTCAGTCACACACAGAGATTCCACACTGGAGGA 720
Qy 906 GAAAGACTAGAGATGCAAGATGCTGTGGAGAGACCTTTAGCCGTGTATTAACCTTAATTCGA 965
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Qy 966 GCAACAAGAGATTCATATGCTGGGAGAAAGCCTTTCGAGTGTAAAGACTGTGGAGAGGC-TT 1024
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RESULT 5
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DEFINITION mRNA sequence.
ACCESSION BM014399
VERSION BM014399.1 GI:16528753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 839)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1AM12062 row: m column: 09
High quality sequence stop: 818.
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Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 39.8%; Score 802.2; DB 3; Length 839;
Best local Similarity 98.8%; Pred. No. 1.8e-217;
Matches 829; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
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Db 61 GTGTGATGAGCTCACTCAGACACAGAGATTCCACACTGGGAGAAAGACTAGATGCA 120
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DEFINITION mRNA sequence.
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VERSION CT001323.1 GI:68295206
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 909)
REFERENCE Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
and Korn, B.
Human T-Lymphocytes library
TITLE

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JOURNAL
COMMENT

Unpublished (2005)
Contract: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPD9016A1714.
RZPDLIB: (Human T-Lymphocytes) RZPD LIB No. 9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016
Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=RZPD9016A1714
contact RZPD (product-support@rzpd.de) for further information.
Primer name: qes 4, Primer sequence: CGGATTAACAATTACACAGC.

FEATURES

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/note="Vector: pQE80LSN_cloned; site_1: SalI; site_2:
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http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - Oligo(dT) primer [5'
GACTGATCTAGATCGCAGCGGCCCTTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN_cloned vector"

ORIGIN

Query Match 37.1%; Score 748; DB 7; Length 909;
Best Local Similarity 98.8%; Pred. No. 5.9e-202;
Matches 770; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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191 AGGTGAGCTAGAGCTCTCGGAATTTGCTTCTTCAAGTGAACCCCGAGAAAGATGATC 250
167 AGTCTTCAAGTCTTAAACAATGAGCCAGAGGTTTGTGACGTTCCGCGACGTAGCCATAG 226
251 AGTCTTCAAGTCTTAAACAATGAGCCAGAGGTTTGTGACGTTCCGCGACGTAGCCATAG 310
227 ACTTTTCTCAGAGAGAGTGGGCTGTGAACTGTGCTTCAAGGAGACCTGTATCGGAGC 286
311 ACTTTTCTCAGAGAGAGTGGGCTGTGAACTGTGCTTCAAGGAGACCTGTATCGGAGC 370
287 TGAATGCTGAGAAACATCAAGTAACTGTGCTCACTGATTTGGAGTCACAGATTAAGAAATA 346
371 TGAATGCTGAGAAACATCAAGTAACTGTGCTCACTGATTTGGAGTCACAGATTAAGAAATA 430
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Db 551 GCTCAGAGGAGGATATGTCATGATGATCATCAATTAATTAATCAAAAGGCTGTACTATA 610
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Qy 587 AGGACTGTGGGAAGGACCTTGTGCTGCTGCTATCACTTAAGTCAATCAGAAAAATCCATA 646
Db 671 AGGACTGTGGGAAGGACCTTGTGCTGCTGCTATCACTTAAGTCAATCAGAAAAATCCATA 730
Qy 647 CTGTGAGAAACCTTATGATTAAGTAAAGATGTAAAGAGCCCTTCGTTGGGCAATCAGC 706
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Qy 707 TTACTCAACATCAAAAAATTCATCTGAGGAGAAAGCCCTTACGATGTAAAGC-TGTGGG 765
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Db 851 AAGCTTTTCATGATGGGCTCAAGCCTCGTTATTCATTAAGAGATCATCTGTGAAAA 908

RESULT 7
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5', mRNA sequence.
ACCESSION BU176917
VERSION BU176917.1 GI:22690901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 915)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsrbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNLMI3497 row: a column: 13
High quality sequence stop: 539.

FEATURES

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ORIGIN

Query Match 36.6%; Score 738.4; DB 5; Length 915;
Best Local Similarity 98.0%; Pred. No. 3.3e-199;
Matches 790; Conservative 0; Mismatches 11; Indels 5; Gaps 4;

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DB 361 ATGTGGAGAGAGCTTATGTCACGCGCCATCAGCTTACACAACATCAGAAAAACGACAGTGG 420
QY 1491 GCGGAAATCTTAAGAAATGTAAAGAGTGTGGAGAGGCGATGTAAACCACTTAACCATCTCG 1550
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QY 1551 AAGAACTCAGAGAGATTCACACAGTGTAAAGAGCCTTTTAAACGCACTAACCCATCTCG 1610
DB 481 AAGAACTCAGAGAGATTCACACAGTGTAAAGAGCCTTTTAAACGCACTAACCCATCTCG 540
QY 1611 CTATGCTTCGCTTTCACAGTGTGTAACTGAGTCAACTGAGTTCAAAAATATATAA 1670
DB 541 CTATGCTTCGCTTTCACAGTGTGTAACTGAGTCAACTGAGTTCAAAAATATATAA 600
QY 1671 TGGAAAAATTCAGAAATTAAGAAATTTTAAAGTCTCAATAGGTGT-GCCCTTGTGAGTAGC 1729
DB 601 TGGAAAAATTCAGAAATTAAGAAATTTTAAAGTCTCAATAGGTGTGCGCTTGTGAGTAGC 660
QY 1730 TGAATGAATCTCTCGGTTCGCGCTCCAGCGCGCGGAGTGAATTCAT-CCCTTGTGTC 1788
DB 661 TGAATGAATCTCTCGGTTCGCGCTCCAGCGCGCGGAGTGAATTCATCCCTTGTGTC 720
QY 1789 CAGCAGATCAGCGCTGTATAGCGCACCAACCTGTAGTACTTAAGCC-GTCTTGTG 1847
DB 721 CAGCAGATCAGCGCTGTATAGCGCACCAACCTGTAGTACTTAAGTAAACGCGCTTGTG 780
QY 1848 GATCA--GATCAACTATCCAGCATC 1871
DB 781 GATCAGGAGATCAACTATGCCAATC 806

RESULT 8
BUS39183 940 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT 10215200 NIH-MGC 107 Homo sapiens cDNA clone
DEFINITION IMAGE:6569870 5', mRNA sequence.
ACCESSION BUS39183
VERSION BUS39183.1 GI:22849624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
            1 (bases 1 to 940)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-f@mail.nih.gov
            Tissue Procurement: ATCC

```

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FEATURES
source
1..940
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6569870"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH-MGC 107"
/note="Organ: breast; Vector: pOTB; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

ORIGIN
Query Match 36.3%; Score 730.6; DB 5; Length 940;
Best Local Similarity 95.9%; Pred. No. 5,7e-197;
Matches 793; Conservative 0; Mismatches 29; Indels 5; Gaps 4;

QY 211 GCCGACGTAGCCATGACCTTTCTCAGAGAGAGTGGCGCTGTGAACCTGTCTAGAG 270
DB 1 GCCGACGTAGCCATGACCTTTCTCAGAGAGAGTGGCGCTGTGAACCTGTCTAGAG 60
QY 271 GACCTGTACTGGGACGTGATGCTGAGAACTACATTAACCTGCTCACTGATTTGAG 330
DB 61 GACCTGTACTGGGACGTGATGCTGAGAACTACATTAACCTGCTCACTGATTTGAG 120
QY 331 TCAGCATATGAAATTAAGAGTTTACCTACAGAAAAAAACATTCATGAATAAGGCTTCC 390
DB 121 TCAGCATATGAAATTAAGAGTTTACCTACAGAAAAAAACATTCATGAATAAGGCTTCC 180
QY 391 AAAAGGATTCAGATGAGAAAGAAATATCCCTTGGCCGCTACTGATATGTAAGGTACG 450
DB 181 AAAAGGATTCAGATGAGAAAGAAATATCCCTTGGCCGCTACTGATATGTAAGGTACG 240
QY 451 CTTGAAAGCCACAGCGCTCCAGAGGAGTATGTCAATCAGATGATCATTAATATGTC 510
DB 241 CTTGAAAGCCACAGCGCTCCAGAGGAGTATGTCAATCAGATGATCATTAATATGTC 300
QY 511 AAAAGGCTGTACTACTAGAGAAAGCAACCCCTCTAGAACATCAGAGATCATTAAGAG 570
DB 301 AAAAGGCTGTACTACTAGAGAAAGCAACCCCTCTAGAACATCAGAGATCATTAAGAG 360
QY 571 AATTCCTTGAATGTAAAGACTGTGGAGAGGCTTTAGTGTGGCTATCACTTAAGTCAA 630
DB 361 AATTCCTTGAATGTAAAGACTGTGGAGAGGCTTTAGTGTGGCTATCACTTAAGTCAA 420
QY 631 CATCAGAAAAATCATATCTGTGAGAAACCTTATGAATGTAAAGATGTAAAGAGCTTTC 690
DB 421 CATCAGAAAAATCATATCTGTGAGAAACCTTATGAATGTAAAGATGTAAAGAGCTTTC 480
QY 691 CGTTGGGGCAATCAGTTTACTCAACATCAAAAAATTCATACTGGGGAGAGCCCTACGAA 750
DB 481 CGTTGGGGCAATCAGTTTACTCAACATCAAAAAATTCATACTGGGGAGAGCCCTACGAA 540
QY 751 TGTAAAGACTGTGAGAGGCTTTTGTATGGGCTCAAGCCTGTATTCATAAGAGATT 810
DB 541 TGTAAAGACTGTGAGAGGCTTTTGTATGGGCTCAAGCCTGTATTCATAAGAGATT 600
QY 811 CATACTGTGAAAAACCTTATGAATGTAAAGACTGTGAGAAAGGCTTTGGGCTGTAT 870

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Db 601 CATACGTGTAAGAAACCTATGAATGAAGAAAGACTGTGAAAGACCTTTGGCGGTGTGAT 660

QY 871 GAGCTCATCTGACACCAAGATTCACACTGGGGGAAAGACTAGATGCAAAACCTGT 930

Db 661 GACCTCACTCAG-ACCAAGA-TCCCACTGGGGGAAAGACTAGAAATGCCACACTGT 718

QY 931 GGGAAAGACCTTTAGCGTGTGTAT-AACTTATTCAGCAAGAGAAATTCATAGTGGG- 988

Db 719 GGGAGACCTTTAGCGCGGTGTATAAACTTATTCGCAAAAGAAATTCATAGTGGGG 778

QY 989 -AGAGCCTTACGAGTGTAAAGACTGTGGGAGGCTTTTATTGTGG 1034

Db 779 AAAAACCTTCCGAGTGTAAAGACTTGGGGGAAAGGCTTTTATTGTG 825

RESULT 9

AM376896/c 756 bp mRNA linear EST 04-FEB-2000

LOCUS IL3-CT0219-271099-022-B04 CT0219 Homo sapiens cDNA, mRNA sequence.

ACCESSION AM376896.1 GI:6881559

VERSION AM376896.1 GI:6881559

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 756)

HCGP <http://www.ludwig.org.br/ORESTES>.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&f2=IL3-CT0219-271099-022-B04&f3=1999-10-27&f4=1>)

Seq primer: puc 18 forward

High quality sequence score: 3

High quality sequence score: 669.

Location/Qualifiers

1..756

Location/Qualifiers

1..756

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="Caxon:9606"

/dev_stage="Adult"

/clone_lib="CT0219"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI. A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 35.6%; Score 718.2, DB 1, Length 756;

Best Local Similarity 98.0%; Pred. No. 1,9e-193;

Matches 738; Conservative 0; Mismatches 13; Indels 2; Gaps 1;

QY 703 CAGCTTACCAACATCAAAATTCATCTGGGAGAGCCCTACGAATGTAAAGACTGT 762

Db 755 CAGCTTTCACACATCAAAA--TTCATATGGGAGAGCCCTACGAATGTAAAGACTGT 698

QY 763 GGGAAAGCTTTTCATAGGCGCTCAAGCCTGTTATTCATTAAGAGATTCTAGTGA 822

Db 697 GGGAAAGCTTTTCATAGGCGCTCAAGCCTGTTATTCATTAAGAGATTCTAGTGA 638

QY 823 AAACCTATGAATGAAGAAAGCTGTGAAAGGCTTTGGCGGTGTGATGACTCACTAG 882

Db 637 AAACCTATGAATGAAGAAAGCTGTGAAAGGCTTTGGCGGTGTGATGACTCACTAG 578

QY 883 CACAGAGATTCACACTGGGGGAAAGACTAGAAATGCAAAAGACTGTGGGAAAGCTTT 942

Db 577 CACAGAGATTCACACTGGGGGAAAGACTAGAAATGCAAAAGACTGTGGGAAAGCTTT 518

QY 943 AGCGTGTGTATTAACCTTATTCAGCAAGAGAAATTCATAGTGGGAAAGCTTTACAG 1002

Db 517 AGCGTGTGTATTAACCTTATTCAGCAAGAGAAATTCATAGTGGGAAAGCTTTACAG 458

QY 1003 TGTAAAGCTGTGGGAAAGCTTTTATTTGTGTGTTTCAAGCTCATTCAGATTAAGAAAT 1062

Db 457 TGTAAAGCTGTGGGAAAGCTTTTATTTGTGTGTTTCAAGCTCATTCAGATTAAGAAAT 398

QY 1063 CACACAGGTGAGAAACCTATGAATGTCAAGAAATGTGGAAAGGCTTTACTGACTCAAT 1122

Db 397 CACACAGGTGAGAAACCTATGAATGTCAAGAAATGTGGAAAGGCTTTACTGACTCAAT 338

QY 1123 TACCTTACTCAGCATCAGAAATTCACACCGGTGAAAGCCTCAGCAATGTAAAGACTGT 1182

Db 337 TACCTTACTCAGCATCAGAAATTCACACCGGTGAAAGCCTCAGCAATGTAAAGACTGT 278

QY 1183 GGGAAAGGCTTTTCGTGGGCTTCAGACCTCGTTAAGCAAGAGGATTCATACGGGCGAG 1242

Db 277 GGGAAAGGCTTTTCGTGGGCTTCAGACCTCGTTAAGCAAGAGGATTCATACGGGCGAG 218

QY 1243 AAGCGTCAAGTGCAGAAATGTGGAAAGGCTTCAATTTGTGCTATCAGCTCAGTCA 1302

Db 217 AAGCGTCAAGTGCAGAAATGTGGAAAGGCTTCAATTTGTGCTATCAGCTCAGTCA 158

QY 1303 CACGAGAGATTCACACAGCGGAAACCCCGTATTAATGTAAAGAGTGTGGAAAGCTTTT 1362

Db 157 CACGAGAGATTCACACAGCGGAAACCCCGTATTAATGTAAAGAGTGTGGAAAGCTTTT 98

QY 1363 ATTTATGATGAGAGCTGTGTAACATGAGAAATTCATACCGGGGTGAACCTATGGG 1422

Db 97 ATTTATGATGAGAGCTGTGTAACATGAGAAATTCATACCGGGGTGAACCTATGGG 38

QY 1423 TGTACAGAAATGTGGGAAAGGCTTTAGTCAAGGC 1455

Db 37 TGTACAGAAATGTGGGAAAGGCTTTAGTCAAGGC 5

RESULT 10

BO719354 890 bp mRNA linear EST 16-JUL-2002

LOCUS AGENCOURT_8291371_lupeki_sympathetic_trunk Homo sapiens cDNA clone

DEFINITION IMAGE:6194787 5', mRNA sequence.

ACCESSION BO719354

VERSION BO719354.1 GI:21858251

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 890)

NIH-MGC <http://mgc.nci.nih.gov/>.

REFERENCE 1

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Stransberg, Ph.D.

COMMENT Email: csagbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLNL13600 row: j column: 04

High quality sequence stop: 556.
Location/Qualifiers

1. 890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6194787"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 Yr"
/lab_host="DH10B"
/clone_lib="lupski, sympathetic trunk"
/note="Vector: PCWV-SPORTS (Life Technologies); Site_1:
Noti; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCACGCGTCG-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN

Query Match 35.3%; Score 711.6; DB 5; Length 890;
Best Local Similarity 98.2%; Pred. No. 1.5e-191;
Matches 752; Conservative 0; Mismatches 9; Indels 5; Gaps 3;

394 AGGAATTCAGATGAGAAAGTAATCCCTTGGCCGTACTGATGATGGAAGTACGCTT 453
1 ATGAATTCAGATGAGAAAGTAATCCCTTGGCCGTACTGATGATGGAAGTACGCTT 60
454 GAAAGCCACAGCGCTCCAGAGGAGTATGTCATCATCATCAATTAATGTCANA 513
61 GAAAGCCACAGCGCTCCAGAGGAGTATGTCATCATCATCAATTAATGTCANA 120
514 AGGCGCTGCTACTAGAGAAAGCACTCCCTCTAGAACATCAGACATCATAGAGAA 573
121 AGGCGCTGCTACTAGAGAAAGCACTCCCTCTAGAACATCAGACATCATAGAGAA 180
574 TCCCTTTGAATGTAAGACTGTGGGAAGGCTTTAGTCGTGCTATCACTTACTCAACT 633
181 TCCCTTTGAATGTAAGACTGTGGGAAGGCTTTAGTCGTGCTATCACTTACTCAACT 240
634 CGAATAATCATATCTGTGAGAAACCTTATGATGTAAGAAAGTAAGAGGCTTCCGT 693
241 CGAATAATCATATCTGTGAGAAACCTTATGATGTAAGAAAGTAAGAGGCTTCCGT 300
694 TGGGGCAATCAGCTTACTCAACATCAAAAATTCATATCTGGGGAAGAGCCCTACGATGT 753
301 TGGGGCAATCAGCTTACTCAACATCAAAAATTCATATCTGGGGAAGAGCCCTACGATGT 360
754 AAAGACTGTGGGAAGGCTTTGCATGGGGCTCAAGCCTCGTTATTCATAAGAGATTCAT 813
361 AAAGACTGTGGGAAGGCTTTGCATGGGGCTCAAGCCTCGTTATTCATAAGAGATTCAT 420
814 ACTGTGTAAGAAACCTTATGATGTAAGAAAGCTTTGGGGCTGTGGTGTGAG 873
421 ACTGTGTAAGAAACCTTATGATGTAAGAAAGCTTTGGGGCTGTGGTGTGAG 480
874 CTCACCTCAGACCAAGATTCACACTGGGGAAGAAAGATCAGATGCAAGAGCTGTGG 933
481 CTCACCTCAGACCAAGATTCACACTGGGGAAGAAAGATCAGATGCAAGAGCTGTGG 540
934 AAAGACTGTGGGAAGGCTTTGCATGGGGCTCAAGCCTCGTTATTCATAAGAGATTCAT 993
541 AAAGACTGTGGGAAGGCTTTGCATGGGGCTCAAGCCTCGTTATTCATAAGAGATTCAT 600
994 CCTTAGAGGTAAAGCTGTGGGAAGGCTTTATTTGTGCTCAAGCCCTATTCAGCAT 1053
601 CCTTAGAGGTAAAGCTGTGGGAAGGCTTTATTTGTGCTCAAGCCCTATTCAGCAT 660
1054 AAAAGATTCACACAGGTGAGAAA--CCCTATGATGTCAAGAA--TGTGGGAAGGCTT 1109

DB 661 AAAAGATTCACACAGGTGAGAAACCTTATGATGTAAGAAAGTGTGGGAAGGCTT 720
QY 1110 TACTGATCAATTAATCTTACTCA--GCATCAGGAAGATCCACACCGG 1154
DB 721 TACTGATCAATTAATCTTACTCAAGGCAATCAGAAATCCACACCGG 766

RESULT 11

CX869347/c 731 bp mRNA linear EST 03-FEB-2005
LOCUS HESCA_34.G02.b1.A037 NIH_MGC_262 Homo sapiens cDNA clone
DEFINITION IMAGE:7474350 3', mRNA sequence.
ACCESSION CX869347
VERSION CX869347.1 GI:58552521
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: HESCA_34.G02.g1.A037
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: BreaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM15782 row: m column: 04
Seq primer: M13-FOR (GTAAACGACGGCCAG)
High quality sequence stop: 704
POLYA=yes.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

1. 731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7474350"
/sex="male"
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/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_262"
/note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BG01.
Positive for Nestin and Musashi expression. Passage number
18. cDNA primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGGAGCGCGCCCT(15)-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalised primary library is
NIH_MGC_259). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below phred quality 16. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Query Match 35.1%; Score 707; DB 8; Length 731;
Best Local Similarity 100.0%; Pred. No. 3e-190;

	Matches	707: Conservative	0: Mismatches	0: Indels	0: Gaps	0: Ns
Qy	1001	AGGTGTAAGACTGTGGGAAAGCCTTTATTTGTGTGTTCAAGCTCATTTACGATATAAAGAA				1067
Db	731	AGGTGTAAGACTGTGGGAAAGCCTTTATTTGTGTGTTCAAGCTCATTTACGATATAAAGAA				672
Qy	1061	TTCAACACAGGTGAGAAACCTTAGATGTCAAGATGTGGGAAGCCTTTACTCGAGTCA				1120
Db	671	TTCAACACAGGTGAGAAACCTTAGATGTCAAGATGTGGGAAGCCTTTACTCGAGTCA				612
Qy	1121	ATTACCTTACTCAGCATCAAAAGATCCACACCGGTGAGAGCTTACAGATGTAAAGAGT				1180
Db	611	ATTACCTTACTCAGCATCAAAAGATCCACACCGGTGAGAGCTTACAGATGTAAAGAGT				552
Qy	1181	GTGGGAAGCCTTTGCTGTGGGGTTTGAGCCTCGTTAAGACAGAGAGATACATACGGGCG				1240
Db	551	GTGGGAAGCCTTTGCTGTGGGGTTTGAGCCTCGTTAAGACAGAGAGATACATACGGGCG				492
Qy	1241	AGAAAGCCGTACAAAGTGCACAGATGTGGGAAGGCCCTTCAATTGTGGCTATCACCTCAC				1300
Db	491	AGAAAGCCGTACAAAGTGCACAGATGTGGGAAGGCCCTTCAATTGTGGCTATCACCTCAC				432
Qy	1301	AGCAGAGAGAAATCCACACAGGCCAAACCCCGTATAAATGTAAAGAGTGTGGAAAGCCTT				1360
Db	431	AGCAGAGAGAAATCCACACAGGCCAAACCCCGTATAAATGTAAAGAGTGTGGAAAGCCTT				372
Qy	1361	TCATTATGATTCGAGCCTCGTGAAACATAGAGAAATTCATTCGCGGGGTGAAACCCCTATG				1420
Db	371	TCATTATGATTCGAGCCTCGTGAAACATAGAGAAATTCATTCGCGGGGTGAAACCCCTATG				312
Qy	1421	GGTGTACAGAAATGTGGGAAGAGCTTTAGTCAAGGCCATCAGCTTACACAACATCAGAAA				1480
Db	311	GGTGTACAGAAATGTGGGAAGAGCTTTAGTCAAGGCCATCAGCTTACACAACATCAGAAA				252
Qy	1481	CGCACAGTGGGGCCGAAATTCCTACGAAATGTAAAGAAATGTGGGAAGGCATGTAAACCACTTA				1540
Db	251	CGCACAGTGGGGCCGAAATTCCTACGAAATGTAAAGAAATGTGGGAAGGCATGTAAACCACTTA				192
Qy	1541	ACCATCTCCGAGAACATCAGAGGATCCACAACAGTTGAAGAGCCTTTGAAAGCAGCAGTAGC				1600
Db	191	ACCATCTCCGAGAACATCAGAGGATCCACAACAGTTGAAGAGCCTTTGAAAGCAGCAGTAGC				132
Qy	1601	CCGCTCCGATCTATAGGTTCGCTTCCACAGTTTGTATCTCGCAATCAACTCGACAGTTCAA				1660
Db	131	CCGCTCCGATCTATAGGTTCGCTTCCACAGTTTGTATCTCGCAATCAACTCGACAGTTCAA				72
Qy	1661	AAATATTAAATGAGAAATTCACGAAATATAAGATTTTAAGTCTCAA 1707				
Db	71	AAATATTAAATGAGAAATTCACGAAATATAAGATTTTAAGTCTCAA 25				
RESULT 12						
LOCUS	CN389062	692 bp	mRNA	linear	EST 16-MAY-2004	
DEFINITION	17000424021726 GRN_ES Homo sapiens cDNA 5', mRNA sequence.					
ACCESSION	CN389062					
VERSION	CN389062.1	GI:47376657				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominoidea; Homo.					
	1 (baaes 1 to 692)					
TITLE	Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,					
	Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,					
	Lebkowski,J and Stanton,L.W.					
JOURNAL	Transcriptome characterization elucidates signaling networks that					
PUBMED	control human ES cell growth and differentiation					
COMMENT	Nat. Biotechnol. 22 (6), 707-716 (2004)					
	15146197					
	Contact: Brandenberger R					
	Regenerative Medicine					

Query Match	33.1%;	Score 666;	DB 7;	Length 692;
Best Local Similarity	100.0%;	Pred. No. 1.5e-178;		
Matches	666;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
FEATURES	<p>Genon Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: tbrandenberg@genon.com Insert Length: 692 Std Error: 0.00. Location/Qualifiers 1..692 "organism="Homo sapiens" "mol_type="mRNA" "/db_xref="taxon:9606" "/issue_type="embryonic stem cells, cell lines H1, H7, and H9" "/clone_lib="GRN ES" "/note="Oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"</p>			
ORIGIN				
Query	47	CAGCCAGCATCTCTTGAGAAAAGCATCCCGAGAGAGAAAGCATGCTTTAA	106	
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Query	107	AGGTCACTCTAGGCTCTGGAAATTGTCCTCTTCACTGAGAAACCCGAGAGACGTATC	166	
Db	87	AGGTCACTCTAGGCTCTGGAAATTGTCCTCTTCACTGAGAAACCCGAGAGACGTATC	146	
Query	167	AGTCTTCAGTTCTTAAACAATGGCCAGGAGTTTGATGACGTTGCCGACGTAGCCATAG	226	
Db	147	AGTCTTCAGTTCTTAAACAATGGCCAGGAGTTTGATGACGTTGCCGACGTAGCCATAG	206	
Query	227	ACTTTTCTCAGAGAGAGATGGGCTGTGAACTCTGCTCAGAGAGACCTGTACTGGAGC	286	
Db	207	ACTTTTCTCAGAGAGAGATGGGCTGTGAACTCTGCTCAGAGAGACCTGTACTGGAGC	266	
Query	287	TGATGCTGAGAACTACAGTAACCTTGGCTCACTGATTTGAGTGCAGCATATGAATA	346	
Db	267	TGATGCTGAGAACTACAGTAACCTTGGCTCACTGATTTGAGTGCAGCATATGAATA	326	
Query	347	AGAGTTTACCTACAGAAAAAACAATTGATAAATAGGCTTCCAAAAGAAATTCAGATA	406	
Db	327	AGAGTTTACCTACAGAAAAAACAATTGATAAATAGGCTTCCAAAAGAAATTCAGATA	386	
Query	407	GAAAGATTAATCCCTTGGCCGATACATGATGATGTAAGGATAGCCTTGAAAGACACAGC	466	
Db	387	GAAAGATTAATCCCTTGGCCGATACATGATGATGTAAGGATAGCCTTGAAAGACACAGC	446	
Query	467	GCTTCAGAGGAGGATATGTCATTCATGATTCATCAATTAATGTCAAAAGGCTGTCTCTA	526	
Db	447	GCTTCAGAGGAGGATATGTCATTCATGATTCATCAATTAATGTCAAAAGGCTGTCTCTA	506	
Query	527	GAGAAAGCACTCTCTCTGAAACATATAGAGACATCTAAGAGAAATTCCTTTGAATGTA	586	
Db	507	GAGAAAGCACTCTCTCTGAAACATATAGAGACATCTAAGAGAAATTCCTTTGAATGTA	566	
Query	587	AGGACTGTGGGAAAGGCTTTAGTGTGGCTATCACTTAATCAACATCAGAAAATTCATA	646	
Db	567	AGGACTGTGGGAAAGGCTTTAGTGTGGCTATCACTTAATCAACATCAGAAAATTCATA	626	
Query	647	CTGTGTGAAACCTTATGAAATGTAAGATGTAAGAAAGGCTTCCGTTGGGGCATCAGC	706	
Db	627	CTGTGTGAAACCTTATGAAATGTAAGATGTAAGAAAGGCTTCCGTTGGGGCATCAGC	686	
Query	707	TTACTC 712		
Db	687	TTACTC 692		

CN389072 696 bp mRNA linear EST 16-MAY-2004
LOCUS 17000424036093 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN389072.1 GI:47376667
ACCESSION CN389072.1 GI:47376667
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 696)
Branderberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G. J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebowicki, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Branderberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbranderberger@geron.com
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H9"
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from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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Query Match 33.0%; Score 664; DB 7; Length 696;
Best Local Similarity 99.9%; Pred. No. 5.8e-178;
Matches 675; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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LOCUS Pan troglodytes ZNF463 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DQ045795
VERSION DQ045795.1 GI:66897010
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
1 (bases 1 to 709)
Nielsen, R., Bustamante, C., Clark, A. G., Gianowski, S., Sackton, T. B.,
Hubisz, M. J., Fedel, A. L., Tanenbaum, D. M., Civeille, D.,
White, T. J., Sniinsky, J. J., Adams, M. D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
15669325
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
Location/Qualifiers
1..709
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/mol_type="genomic DNA"
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<1..>709
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/locus_tag="HC11559"
ORIGIN
Query Match 32.9%; Score 663.2; DB 11; Length 709;
Best Local Similarity 93.8%; Pred. No. 9.8e-178;
Matches 665; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 692 GTTGGGGCAATGACCTTACTCAACATCAAAAATTTCTACTGTGGGAGAGCCCTACGAT 751
DB 1 GTTGGGGCAATGACCTTACTCAACATCAAAAATTTCTACTGTGGGAGAGCCCTACGAT 60
QY 752 GTAAGAGCTGTGGGAGAGGCTTTTGCATGGGGCTCAAGCCTGTTATTCAATAGAGATTTC 811
DB 61 GTAAGAGCTGTGGGAGAGGCTTTTNNNATGGGGCTCAAGCCTGTTATTCAATAGAGATTTC 120

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857 TTCGGGCTGTGTAGAGTCACTCAGCACCAGAGATTTCCACTGTGGGAGAAAGACTAG 916
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1450 TTCATAGTGGGGAGAAAGCCTTACAGATGTAAAGCTGTGGAGAGGCTTTATTTGGT 1509
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1217 AGCACAAGAGATATACCGGGGAGAGAGCCTTACAAGTCAAGATGTGGAGAGGCTT 1276
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RESULT 2

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US-11-112-908-55
; Sequence 55, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

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Query Match 23.9%; Score 482.4; DB 8; Length 193789;

Best Local Similarity 65.9%; Pred. No. 8.2e-142;

Matches 699; Conservative 0; Mismatches 361; Indels 0; Gaps 0;

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US-11-000-688-419
; Sequence 419, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUDGATTE, Remi
; APPLICANT: BIRBAUD, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688

; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 419
; LENGTH: 3198
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc feature
; LOCATION: (1)-(3198)
; OTHER INFORMATION: hypothetical protein mgc13071 (MGC13071)
; OTHER INFORMATION: gene.
US-11-000-688-419

Query Match 23.3%; Score 468.8; DB 8; Length 3198;
Best Local Similarity 66.9%; Pred. No. 1.2e-138;
Matches 682; Conservative 0; Mismatches 337; Indels 1; Gaps 1;

QY 568 GAGAAATTCCTTGAATGTAAAGACTGTGGAGAGCCTTTAGTGTGCTATCACTTACT 627
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Db 721 GCAAGCCTTGCCCATCATTAAGAGATTCATCTGTTCAAAACCTTTGAATGTAAAGAG 780

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 QY 1468 CAACATCAGAAAAACGACAGTGGGGGAAATCCTACGAAATGTAAAGAGTGGGAAAGGCA 1527
 DB 901 ATACATCGACAGATTCTATCTGCTGAGAAACCTTAAGAAATGTAAAGAAATGTGGGAAAGGCC 960
 QY 1528 TGTAAACCACTTAACCATCTCCGAGAACATCAGAGGATCCACAACAGTTGAAAGGCTTT 1587
 DB 961 TTTAGTATCTGACACTTACTACTGACATCTGAGTATTCACAGTGTAAAGAGACCTTTT 1020

RESULT 4

US-10-750-185-44166/c
 ; Sequence 44166, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 44166
 ; LENGTH: 4305
 ; TYPE: DNA
 ; ORGANISM: Bovine 1986680546157
 ; US-10-750-185-44166

Query Match 22.1%; Score 444.6; DB 7; Length 4305;
 Best Local Similarity 64.3%; Pred. No. 7, 8e-131;
 Matches 659; Conservative 0; Mismatches 384; Indels 4; Gaps 2;

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 DB 3523 AACCATATGATGTAGTGAAGTGTGGGAGGCTTTCAACCAAGTCAACCTTGTCCAGG 3464
 QY 547 ACAATCAGAGATCATTAAGAGAAATCTTTGATGTAAAGACTGTGGGAAAGGCTTT 606
 DB 3463 AC-CAGAGATACACCCGAGAAAACTATTGTAAGTAAGAAATGTAGGAAAGGCTTC 3405
 QY 607 AGTCGCGCTATCACTTATGTCAACATCAGAAATCCATATCTGTGAGAAACCTTAGAA 666
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DB 3164 GGAAGGCTTTTCAGGACAGACATCGCTTATCCCTCACTGGAGATATATATCACTGGG 3105
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 DB 3104 GAGAAACCTTTGACTGTATGATCTGTGTGCAAGGCTTCAGGATCACTAGACTTAT 3045
 QY 964 CAGCAAGAGAAATTCATATGTGGGAGAAAGCTTACAGTGTAAAGACTGTGGGAAAGCT 1023
 DB 3044 CAGCAGAGAGATTCATATCTGAGAGAAACCTTAATTAATGTGTGTGGGAAAGCC 2985
 QY 1024 TTTATTTGTGTTCAAGCTTCATCAGATTAAGAAATTCACACAGTGTGAAACCTTAT 1083
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 QY 1084 GAATGTCAAGAAATGTGGGAAAGGCTTTTACTGAGTCAATTCATTCATCAGATCAGAA 1143
 DB 2924 GAATGTCAATCTGTGGGAAAGCTTTCAGCCATTCATCTCCTCACTCACCCAGCAACAA 2865
 QY 1144 ATCCACACCGGTGAGAAAGCTTCACGAAATGTAAAGAGTGTGGGAAAGGCTTTGCTGGGT 1203
 DB 2864 GTGCAATTCGTGAGAGAAAGCTTACCAATGCAAGGAAATGTGAAAGCTTTCAAGGACAG 2805
 QY 1204 TCGAGCTTCGTTAAGACAGAGATCATATACGCGCAGAAAGCTTCAAGTCAAGAA 1263
 DB 2804 ATACACCTTGTAGCCATCTGAGATTCATCTGAGAGAAACCTTATGAATGTAAAGAA 2745
 QY 1264 TGTGGGAAAGGCTTCAATTTGTGCTATCACTCAGTCCAGAGAGAAATCCACAGGCT 1323
 DB 2744 TGTGAAAGGCTTTTATGATCATGTTCAAGCTGTGCTATCTCAACAGAAATTTATCTGGA 2685
 QY 1324 GAAACCCGTATTAATGTAAAGAGTGTGGGAAAGGCTTTCAATTTATGATGAGCCTGTG 1383
 DB 2684 GAGAAACCTTATGAATGTAAAGAAATGCGGAAAGGCTTCAACAGAGGCAATCTCGCA 2625
 QY 1384 AAACATGAGAAATTCATCCGGGTGAAACCTTATGTGTGACAGAAATGTGGGAAAGG 1443
 DB 2624 CAGCACATTAATTAATCATCTGTGAGAGAAACCTTACATGTGATCTGAAATGTGTAAGCC 2565
 QY 1444 TTTATGTCAGGCTATCAGCTTTCACACATCAGAAAGCAAGTGGGGCGAAATCTTAC 1503
 DB 2564 TTGAGCCAGCTTACCCGCTTATTCACATCTCAGAGATTTCAACAGAGAGAAAGGCTTAT 2505
 QY 1504 GATGTAAAGAGTGTGGGAAAGGCAATGTAAACCACTTAACCTCCGAGAAATCAGAG 1563
 DB 2504 GATGTCAAGATGTGGGAAAGGCTTTTATGTACAGTCACTCCGTGCTCAGATCTGAGA 2445
 QY 1564 ATCCACA 1570
 DB 2444 CTTTACA 2438

RESULT 5

US-10-750-623-44166/c
 ; Sequence 44166, Application US/10750623
 ; Publication No. US20050287531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-1
 ; CURRENT APPLICATION NUMBER: US/10/750,623
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 44166

LENGTH: 4305
 TYPE: DNA
 ORGANISM: Bovine 19866880546157
 US-10-750-623-44166

Query Match 22.1%; Score 444.6; DB 7; Length 4305;
 Best Local Similarity 64.3%; Pred. No. 7.8e-131;
 Matches 699; Conservative 0; Mismatches 384; Indels 4; Gaps 2;

QY 487 AATCAGATATCATCATTAATATGTCAAAGGCTGTCTACTAGAGAGGCAACCTCTTAGA 546
 DB 3523 AACCATATGAGTGAAGACTGTGGAGAGGCTTCAACCAAGATCAACACTTGTCTCAGC 3464
 QY 547 AACATCAAGACATCATTAAGAGAAATTCCTTGAATGAAGACTGTGGAGAGGCTTT 606
 DB 3463 AC-CACAGAAATCACACCGGAGAAAACTATTGTAAGAAATGTAGGAAAGCTTTC 3405
 QY 607 AGTCGTGCTATCAACTTATGTCAACATCAAGAAATCCATCTGTGAGAAACCTTATGAA 666
 DB 3404 AGCCAAAAATGTACATCTTTTCAACATCAAGAAATTCATCTGAGAAAAACCATTTAA 3345
 QY 667 TGTAAAGAAATGAAGAGGCTTCCGTGGGCAATCACTTACTCAACATCAAAAAAT 726
 DB 3344 TGTAAAGAGTGAAGAAAGCTTCAAGCCAGCTGCACACTGTCTCAGCATCAGAAATT 3285
 QY 727 CATCTGGGGAGAAAGCTTACGAATTAAGACTGTGGAGAGGCTTTGATGGGCTCA 786
 DB 3284 CATCTGGGGAGAAAGCTTATTAATTAAGAAATGTGGAGAGGCTTCAAGTATGCTCG 3225
 QY 787 AGCTGTGTAATTCATTAAGAGATTCATCTGTGTAAGAAACCTTGAATGAAGACTGT 846
 DB 3224 TCTTTTGGCCGACATGAGAGTGTCACTGGCAAAAGCCGTACAAATGTATGAAATG 3165
 QY 847 GGAAGAGCTTTGCGGTGTGTAGCTCACTCAAGACCAAGAGA--TTCCACTGTGG 903
 DB 3164 GGGAAAGCTTTGAGGAGAAACATGCTTATCCGTCACTGAGATTAATATCACTGGG 3105
 QY 904 GAGAAAGACTAGGAATGCAAAAGCTGTGGAGAGACCTTTAGCCGTGTGTATTAACCTTAT 963
 DB 3104 GAGAAAGCTTTGACATGCACTGTGTGGCAAGGCTTCAAGCATCAATAGAACTTAT 3045
 QY 964 CAGCACAAGAAATTCATGTGTGGAGAGGCTTCAAGTGTAAAGACTGTGGAGAGCT 1023
 DB 3044 CAGCACAAGAGATTCATCTGAGAGAAACCTTAAATGTATGTGTGTGGAGAAAC 2985
 QY 1024 TTTATTTGTGTCAAGCTCATTCATGCAATAAAGATTCACACAGTGAAGAAACCTTAT 1083
 DB 2984 TTCAGTACGGCTCATCCCTGACCGTCACTCAGAAATTCACAGAGAGAAACATAT 2925
 QY 1084 GAATGTCAAGATGTGGAGAGGCTTTTCTCGAGTCAATTAACCTTCTCAGCATCGAAG 1143
 DB 2924 GAATGTGAATCTGTGGAGAAAGCTTCAAGCATCATGCTCACTCAACGAGCAAAAG 2865
 QY 1144 ATCCACACCGGTGAGAGGCTCAAGATGTAGAGAGTGGAGAGGCTTTGCTGGGGT 1203
 DB 2864 GTGCATTTCTGAGAGAGGCTTCAATGCAATGAGAGAAATGTGGAGAAACCTTCAAGG 2805
 QY 1204 TCGAGGCTGTGAAGCAGAGAGATCAATACGGGAGAGAGGCTTCAAGTGCACAGAA 1263
 DB 2804 ATACACCTTGCTAGCATGTGAGATCAATACGAGAGAAACCTTATGAATGAAGAA 2745
 QY 1264 TGTGGAGAGGCTTCAATGTGTGCTATCACTCACTCAGCAGAGAGATCCACAGAGG 1323
 DB 2744 TGTGGAGAGGCTTTTGAATCAATGCTTCAAGCTGTGCTATCATAGAGAAATTCATCTGA 2685
 QY 1324 GAAACCCGTATTAATGAAGAGTGTGGAGAGGCTTTCAATTAATGATCGAGCTCTGTG 1383
 DB 2684 GAGAAACCTTATGAATGAAGAGTGTGGAGAGGCTTCAACAGAGGAGCATCTTCGA 2625
 QY 1384 AAACATGAAGAAATTCATCCGGGTGAAGCCCTTATGGGTGTCAGAAATGTGGAGAGG 1443
 DB 2624 CAGCACAATTAATTCATCTGAGAGAGAAACCTTATGATGTACTGAATGTGTAAAGCC 2565

QY 1444 TTTAGCAGGCGCATCAGCTTACAGAACATCAGAAAAACGACAGTGGGCGAAATCTTAC 1503
 DB 2564 TTCAAGCAGGCTTACCGGCTTATTCACATCAGAGAGTTCAACAGAGAGAAAGCTTAT 2505
 QY 1504 GAATGTAAAGAGTGGGAGAGGAGCATGTAAACACTTAACATCTCCGAGAACATCAGAG 1563
 DB 2504 GAATGCATGAATGTGGAGAGGCTTTTATGTACAGCTCATCCGTCTCAGCATCTGAGA 2445
 QY 1564 ATCCACA 1570
 DB 2444 CTTCACA 2438

RESULT 6
 US-10-750-185-49223

Sequence 49223, Application US/10750185
 Publication No. US20050260603A1
 GENERAL INFORMATION:
 APPLICANT: NMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: COMPOSITIONS FOR INHERITING BOVINE TRAITS
 FILE REFERENCE: M011100-2
 CURRENT APPLICATION NUMBER: US/10/750,185
 PRIOR FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 49223
 LENGTH: 1730
 TYPE: DNA
 ORGANISM: Bovine 19866880440784
 US-10-750-185-49223

Query Match 21.8%; Score 439.6; DB 7; Length 1730;
 Best Local Similarity 63.2%; Pred. No. 1.7e-129;
 Matches 707; Conservative 0; Mismatches 409; Indels 2; Gaps 2;

QY 528 AGAAGGCAACCTCTCTAGAACATCAGAGA-CATCATTAAGAGAAATTCCTTGAATGA 586
 DB 130 AAGATTCATCCCTTGTCTAAACATGAGAAATCATTCGAAAGAGCCCTTGAATGA 189
 QY 587 AGAAGTGTGGAGAGGCTTTAGTGTGCTATCACTTAAGTCAACATCAGAAATCATATA 646
 DB 190 ATCACTGTGAGAAATCTTCAAGTTGAGGCTTCATCTTGTGCAATCAGAGAACTCAT 249
 QY 647 CTGTGTAGAAACCTTATGAATGTAAAGAAATGTAAAGAGGCTTCCGTGGGCAATCAGC 706
 DB 250 CAGGGGAGAAACCTTATGAATGTAAATGAATGTGGAGAAATCATTCAGCCGACCTCACC 309
 QY 707 TTACTCAATCAAAAAATTCTA-CTGGGAGAGGCTTAAAGATGTAAAGACTGTGG 765
 DB 310 TTGTTCCTCATAAAGAACTCATCTGAGAGAAACCTTACAGAGTATCATGATGTGT 369
 QY 766 AAGGCTTTGATGGGGCTCAAGCTGTATTTCAATTAAGAGATTCATCTGTGAAAAA 825
 DB 370 AATCTTTTACGACAGAGCTATGTCTTGTGTGATCAGAGAACTCATCTGAGAGAG 429
 QY 826 CCTTATGAATGTAAAGACTGTGAAAGGCTTTGCGGTGTGTAGTCACTCAGCAC 885
 DB 430 CTTTACGAGTGAATCAGAGTGTGAAAGTCAATCAGACAGCTCAAACTTATTCGACAT 489
 QY 886 CAGAGTTTCAACATGGGAGAGAAAGATCAAGATCAAGACTGTGGAGAGGCTTTTAC 945
 DB 490 CAAAGAACTCATCTGAGAGAGGCTTACAGATGTAAATGTGGAGAAATCATTTATC 549
 QY 946 CGTGTGTATTAATTCATTCAGCAAGAGAAATTCATAGTGGGAGAGGCTTACAGAGT 1005

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Db      550 CAGAGCTATAACTTATGCCCATCAAGAAATTCATCTGAGAGAAAAGCCCTATGAAATGC 609
QY      1006 AAAGACTGTGGAGAGCTTTTATTTGTTGAAGCCTCATTCAGCATAAAGATTCAC 1065
Db      610 AATCAATGTGGAAAGCTTTTATAGTCAAAAGTTACAACTTGTCCACAGAGAACTCAC 669
QY      1066 ACAGGTGAGAAACCTTATGAAATGTCAGAAATGTGGAAAGCCTTTA CTCGAGTCAAATTAC 1125
Db      670 ACAGGAGAAAACCTTTGAAATGTAATCAAGTGTGAGAAAATCTTCAGCTGAGACTCTCAA 729
QY      1126 CTTACTCAGATGAGAAATCCACACCGGTGAGAAAGCTTCACGAATGTAAAGAGTGTGG 1185
Db      730 CTGTGTGACACCAAGAACTCACTGTGAGAGAAACCTTACGAATGTAAATGTGTGG 789
QY      1186 AAGGCTTTTCGTGGGGTTCGAGCCTCGTTAAAGCAGAGAGATATACAGCGGCGAGAAAG 1245
Db      790 AATCTTTTCAACCGCAGTTTCTACCTTTTATGATCAGAGAACTCACTGAGAGAAAA 849
QY      1246 CCGTACAGTGACAGAAATGTGGAAAGCCTTCAATTTGGCTATCACTCACTCAGCAC 1305
Db      850 CCTATGAATGTAAACAGTGTGGAAAGTCTTCAGCAGAGTTATGCTTGTGTATCAT 909
QY      1306 GAGAGAAATCCACAGAGCGAAACCCGCTATAATGTAAAGATGTGGAAAGCTTTCAAT 1365
Db      910 CAGAGAACTCACTGCGCGAAAGCCCTATGAGTGAAGTGAATGTGAAATCTTCAG 969
QY      1366 TATGATTCGAGCCTCGTGAACATGAGAAATTCATACCGGGGTGAACCCCTATGGGTGT 1425
Db      970 CAGAGTTCAATGCTTACTCAACATCAGAGAACTCATCTGAGAGAAACCCCTATGAAATGT 1029
QY      1426 ACAGAAATGTGGAGAAAGCTTTAGTCAAGCGCATCACTTACACACATCAGAAAGCGCAC 1485
Db      1030 AATCAATGTGGAAACCAATTCAGCTTGAAGTCTCGACTTATGTATCATCAAGAACTCAT 1089
QY      1486 AGTGGGGCCAAATCCATACGAATTAAGAGATGTGGGAGAGCATGTAAACCACTAAACCAT 1545
Db      1090 ACTGAGAGAAACCTTTTACGTAAATCAATGTGGGAAAGCTTTCAATTAATGTTCTTAA 1149
QY      1546 CTCGGAACATCAGAGATCCACAACAGTTGAAGAGCCTTTGAAACGAGTACCGCGCT 1605
Db      1150 CTATATTAGACATGAGCAACTCATACGAAGAGAAACCTTATGATGTAACTAGCTCGA 1209
QY      1606 CGTATCTATGCTTTCGCTTCCACAGTTGTAACTGCG 1643
Db      1210 AATCTTTCAAGAGAGATATCCCTTCCTCCTGCTCC 1247

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RESULT 7

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US-10-750-623-49223
; Sequence 49223, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MW11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49223
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Bovine 19866880440784
US-10-750-623-49223

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Query Match      21.8%; Score 439.6; DB 7; Length 1730;
Best Local Similarity 63.2%; Pred. No. 1.7e-129;
Matches 707; Conservative 0; Mismatches 409; Indels 2; Gaps 2;

QY      528 AGAAGGCAACCCCTCTAGAACATCAGAGA-CATCATAGAGAAATTCCTTGAATGA 586
Db      130 AAGATTCAATCCCTTGTCTCAAAACATGAGAAATCATTCGAAAGAAAGCCCTTTGAATGA 189
QY      587 AGGACTGTGGAAAGCCTTTAGTCGTGCTATCAACTTATAGTCAACATCAGAAAATCCATA 646
Db      190 ATCAAGTGTGAAAATTCCTTCATTTGAGAGCTCATCTTGTTCATCATCAGAGAACTCAT 249
QY      647 CTGTGTGAAACCTTATGAAATGTAAAGAAATGTAAAGAGCCTTCCGTTGGGCAATCAGC 706
Db      250 CAGGGGAGAAACCTTATGAAATGTAAATGTAAATGTGGGAAATCATTTACGCCCACTCTCAC 309
QY      707 TTACTCAATCAAAAAAATTCATA-CTGGGGAGAAAGCCCTAGGAATGTAAAGATGTGGG 765
Db      310 TTGTTTCCCATCAAGAACTCATACCTGAGAGAAACCTTACAGATGTAAATCATGTGTGT 369
QY      766 AAGGCTTTTCGATGGGGCTCAAGCCTCGTTATTCATTAAGAGATTCATCTGTGAAAA 825
Db      370 AATCCTTTAGCCAGAGCTATGTCTTGTGTGATCAGAGAACTCATCTGAGAGAAAG 429
QY      826 CCTATGAATGTAAAGACTGTGAAAAGCCTTTCCGCGTGTGTGATGAGCTCACTCAGCAC 885
Db      430 CCTTACAGAGTGAATCAGTGTGAAAAGTCAATTCAGACAGCTACAACTTATCGCACAT 489
QY      886 CAGAGATTCACATCGGGGAGAAAGCTACGAAATGAAAGACTGTGGGAAAGCCTTTAGC 945
Db      490 CAAGAACTCATCTGAGAGAAAGCCCTACGAATGTAAATCAATGTGGGAAATCATTTATC 549
QY      946 CCGTGTATATAACTTATTCAGACAAAGAAATTCATAGTGGGAGAAAGCCTTACAGAGTGT 1005
Db      550 CAGAGTATAAATCTTATTCCTCATCAAGAAATTCATACGTGAGAAAGCCCTATGAAATGT 609
QY      1006 AAGACTGTGGAGAGCCTTTTATTTGTGTCAAGCCTTATTCAGATATAAAGATTCAC 1065
Db      610 AATCAATGTGGAAAGCTTTTATGTCAAAAGTTCAAACTTGTGCCCCACAGAACTCAC 669
QY      1066 ACAGGTGAGAAACCCCTATGAATGTCAAGAAATGTGGGAAAGCCTTTTACATGAGTCAATTAC 1125
Db      670 ACAGGAGAAAACCTTTGAATGTATCAAGTGTGAAAATCCTTCAGCTGAGACTCTCAA 729
QY      1126 CTTACTCAGATCAGAGATCCACAACCGGTGAGAAAGCTTCAGAAATGTAAAGAGTGTGG 1185
Db      730 CTGTGTGACACCAAGAACTCACTGTGAGAGAAACCTTATGATGTAAATGATGTGG 789
QY      1186 AAGGCTTTTCGTGGGGTTCGAGCCTCGTTAAAGCAGAGAGATATACAGCGGCGAGAAAG 1245
Db      790 AATCTTTCAACCGCAGTTCTCACTTGTATGCAATCAGAGAACTCACACTGAGAGAAAA 849
QY      1246 CCGTACAGTGACAGAAATGTGGGAAAGCCTTCAATTTGGGCTATCACTCACTCAGCAC 1305
Db      850 CCTATGAATGTAAACAGTGTGGAAAGTCTTCAGCAGAGTTATGCTTGTGTATCAT 909
QY      1306 GAGAGAAATCCACAGAGCGAAACCCGCTATAATGTAAAGATGTGGGAAAGCCTTTCAAT 1365
Db      910 CAGAGAACTCACTGCGCGAAAGCCCTATGAGTGAAGTGAATGTGAAATCTTCAG 969
QY      1366 TATGATTCGAGCCTCGTGAACATGAGAAATTCATACCGGGGTGAACCCCTATGGGTGT 1425
Db      1426 ACAGAAATGTGGAGAGCCTTTAGTCAAGCCCATCACTTACCAACAATCAGAAAGAGCAC 1485
QY      1030 AATCAATGTGGAAACCAATTCAGCTTGAAGTGTCACTTATGTATCATCAAGAACTCAT 1089
QY      1486 AGTGGGGCAAAATCCATCAAGATGTAAAGATGTGGGAAAGCATGTAAACCACTTAAACCAT 1545
Db      1090 ACTGAGAGAAACCTTTTACGTATATCAATGTGGGAAAGCTTTCAATTAATGTTCTTAA 1149
QY      1546 CTCGGAACATCAGAGATCCACAACAGTTGAAGAGCCTTTTGAAGCAAGTACCGCGCT 1605

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Db      1150 CTTATTAGCATCAGGCACTCATACAGAGAAAACCTTAGATGTAATGACTGGA 1209
Qy      1606 CGTATCTATGTTTGGCTTTCACAGTTTGTACCTGC 1643
Db      1210 AATCTTTCAGAGAGATATCCCTTCCCTTGCCTCC 1247

RESULT 8
US-10-775-169-119
; Sequence 119, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorneier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 119
; LENGTH: 5871
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-119

Query Match      20.9%; Score 421.4; DB 7; Length 5871;
Best Local Similarity 62.4%; Pred. No. 2.4e-123;
Matches 676; Conservative 0; Mismatches 406; Indels 1; Gaps 1;

Qy      506 ATGTCAAAAGGCGTGTACTAGAGAAAGCAACCCCTCTAGAACATCAGACATCATATA 565
Db      508 AAGTCAGAGAGAAACATATTTCTGAACCTTCTTCTGCTTCAAGAGAGCTCATTA 567
Qy      566 -AGGAAATTCCTTGAATGTAAAGACTGTGGAAAGCCCTTATGTCGTATCAACTT 624
Db      568 GAGGGGGAAGCCAAATCCTTGGCATATCTGTGGCAAAACCTTCACTTATTCGAGCTTA 627
Qy      625 AACTCAATCAGAAAATTCATATCTGTGAGAAACCTTATGATGTAAAGATGTAAAG 684
Db      628 GTTAAAGCATGTGATTTGGATCTGTGGAGAAACCTTAACTGCGATCAGTGTGGAAA 687
Qy      685 GCCTTCGGTTGGGCAATCAGCTTACTCAACATCAAAAATTCATCTGGGAGAAAGCC 744
Db      688 GCGTTTGGCCAGAGCTCAACCTTATGAGCATCAGAAATTCACACTGGAAGAGACTC 747
Qy      745 TACGAATGTAAAGACTGTGGAAAGCTTTTCAGATGGGCTCAAGCCTGTATTCATAAG 804
Db      748 TACGCTGTAAATGTGTGGAAAGACTTCATTCACTATTCAGTCTCATTTGAGCATCAG 807
Qy      805 AAGATTCATACGTGTGAAAACCTTATGATGTAAAGATGTGAGAAAGCCCTTGGGCT 864
Db      808 CCGCTTCATTCAGAGAAAGCCCTTCAATGTGCGCATGTGGAGAGCGCTTTTGTCCAC 867
Qy      865 GGTGATGAGCTCAGTCAGACAGAGATTCACAACCTGGGAGAAAGATCAAGATGCACA 924
Db      868 AGTTTCAAGCTGATTAAGCACCAGAGAGCTTACACAGAGAGAGACTTGTGAATGCACA 927
Qy      925 GACTGTGGAGAGACCTTTAGCCGTGTATTAACCTTATTCAGACAGAGAAATTCATAGT 984
Db      928 GAGTGTGGAGAAAGGCTTTCAGTCAGAGCTCTTATCTTATTCGCATCAGAGATTCACAG 987
Qy      985 GGGGAGAGACCTTACAGAGTGTAAAGCTGTGGAGAGGCTTTTATTTGTGCTCAAGCCCTC 1044
Db      988 GAGAGAAAGCCCTTATGAGTGCATGATGTGGAAATCTTCAITAAAGAGCTCGAGCCCTC 1047
Qy      1045 ATTCAAGCATTAAGATTCACACAGGTGAGAAACCTTATGAAATGTCAAGATGTGGAG 1104
Db      1048 ATTGCGCATTTACATGATCACAAGAGAGTGAACGTAATGAAATGCAAAAGATGTGGAG 1107

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Qy      1105 GCCTTACTCGAGTCAATTTACTTACTGAGATCAGAAATGCCAGCCGTGAGAAAGCT 1164
Db      1108 GCATTCGCTCATCGTCTGACAGCTTATTTGAACACAGAAATTTACACCGAGAGAGACCC 1167
Qy      1165 CACGAATGTAAAGAGTGTGGAGAGGCTTTCGCTGGGGTTCGAGCCTGTTAAGACAGAG 1224
Db      1168 TTGGAATGCATGATGTGTGGAAAGCTTTATTCGAGAGTTCAAAGCTCATTCAGATCAG 1227
Qy      1225 AGGATATCATACGGGCGAGAAAGCCGTACAGATGCACAGAAATGTGGAAAGGCTTCAATTGT 1284
Db      1228 AGATTCATTACTGGGAGAGGCTTACGATATCATGATGTGGAAAGGCTTTCAGCCAG 1287
Qy      1285 GCGTATCACTTCACTCAGCAGAGAGATTCACACAGCCGAAACCCCGTATTAATGTAG 1344
Db      1288 ACGTAAACCTTCAACCCAGCATCAGAAATTCACCTGAGAGAAACTGTATAAATGTAAAC 1347
Qy      1345 GAGTGTGGAAAGGCTTTCATTTATGATCGAGCCTGTGAAACATGAGAAATTCATACC 1404
Db      1348 GAGTGTGGAAAGGCTTTCCTTCTGTGATTCATACCTTATTCACACAGAAATTCACACT 1407
Qy      1405 GGGGTGAAACCTTATGGTGTACAGAAATGTGGAAAGCCTTTAGTCAGGCGCATCAGCTT 1464
Db      1408 GGAGAGAGAGTGTATGAAATGTGAAGATGTGGAAAGGCTTCTCCAGAAAGCCATCTC 1467
Qy      1465 ACACAACATCAGAAACCGCACAGTGGGCGAAATCTTACGAATGTAAAGATGTGGAGAG 1524
Db      1468 ACTGAGCACCAAGAAATCCTCTGTGGAGACAGCCCTTCAATGTAAAGATGTGGAGAA 1527
Qy      1525 GCATGTAAACCACTTAAACATCTCCAGAAACATCAGAGGATCCACAGTTGAAGAGCC 1584
Db      1528 GCTTCATTCAGAGCTTCCAGCTGCTTCTGACACGAAATTTACACATCGAGAGAAAGCC 1587
Qy      1585 TTT 1587
Db      1588 TAT 1590

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RESULT 9
US-10-750-185-56682/c
; Sequence 56682, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 56682
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56682

Query Match      20.5%; Score 413.8; DB 7; Length 934;
Best Local Similarity 68.0%; Pred. No. 1.9e-121;
Matches 591; Conservative 0; Mismatches 277; Indels 1; Gaps 1;

Qy      550 CATCAGACATCATTAAGAGAAATTCCTTTGAATTAAGAGCTGTGGAGAGCCCTTTAGT 609
Db      875 CAGAAAATTCATCATGATGTGAACCTTATATCTGTAAAGATGTGAAAGGCTTTTGGT 816
Qy      610 CGTGCATATCAACTTAATGATCAAGAAATTCATATCTGTGTGAGAAACCTTATGAAATGT 669

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Db      815 CATCATTCAGTCTCTATCAACCAAGAAATTCATTCTGTGAGAAACCATTAATGT 756
Qy      670 AAAGAAATGAAGAGGCTTCCTGTTGGGGCAATCAGCTTACTCAATCAAAAATTCAT 729
Db      755 AAACAGTGTGAAGAGGCTTTGTTTACAGTATCTCTTACTAACAACAGAAAGTCAAT 696
Qy      730 ACTGGGAGAGGCTTCAGATGTAAAGCTGTGGAGAGGCTTTTGCATGGGCTCAAG 789
Db      695 ACTGGTGAAGGCTCATGATGTAAAGATGTGAAGAGGCTTTGTAGGGCTCAAG 636
Qy      790 CTCGTATTCATTAAGAGATTCATCTGTGAAAAACCTTAATAAGTAAAGCTGTGA 849
Db      635 CTTCCTTAAGACTTAAGAGATTCGTAGTGTGAAGAAACATATATGTGAAGATGTGG 576
Qy      850 AAGGCTTTTCGGGCTGTGTAGTCACTCAGACACAGAAATTCACACATGGGGAGAA 909
Db      575 AAGGCTTTCTGTAGATTTATCAATTTACAAACATCAGAAATTCATCTGTGTGAAG 516
Qy      910 GAATCAAGATGCAAGAACTGTGGAGAACTTTAGCCGTGTATTAACCTTATTCAGAC 969
Db      515 CCCATGAATGTAAAGATGTGGAGAACTTTAAGCTCATCTTAACCTTATTAACAT 456
Qy      970 AAGAGATTCATAGTGTGGAGAACTTTAGAGATTAAGACTGTGGAGAGGCTTTTAT 1029
Db      455 CAGATCAATTCACAGTACTTGAACCATATGAATGTAAACATGTGGAGAGGCTTCAAT 396
Qy      1030 TGTGTTTCAAGCCTCATTCAGCATTAAGAAATTCACACAGTGAAGAAACCTTATGA 1089
Db      395 CGTGTGGGAGAACTTTAAATGCATGATCAATTCATCTGGGAGAAACCTTATGAATGT 336
Qy      1090 CAAGAAATGTGGAGAGGCTTTACTCGATCAATTAACCTTACAGCATCAAGAAATCCAC 1149
Db      335 AAGGAATGTGAAGAAACCTTTAAGCTTAATTTCTAAATATATCATCAGCAGATCCAT 276
Qy      1150 ACCGTGAGAAAGCTTCAGAAATGTAAAGATGTGGAGAGGCTTTTGGCTGGGTTGAGC 1209
Db      275 ACTGGCTTGAACCATATATATGTAAAGATGTAAAGAGGCTTTCCGTCTATATACAGT 216
Qy      1210 CTCGTTAAGCAGAGAGATACATACGGGCG-AGAAAGCGTACAGAGACAGAAATGTGG 1268
Db      215 CTTCCTCAACATTAAGAAATTCATCTGTGAAAAAACCTTTATGATGTAAAGAAATGTGG 156
Qy      1269 GAAGGCTTCAATTTGTGCTATCACTCACTCAGACAGAGAAATCCACAGGCGAAAC 1328
Db      155 TAAGGCTTTAATCGTAGCGAGGACTTATTCAGCATCAGAAATTCATCTGCGTGA 96
Qy      1329 CCGGTATTAATGTAAAGAGTGTGGAGAGGCTTTCACTTATGATTCAGGCTCGTGAACA 1388
Db      95 GCCACATTAATGTACGAAATGCGGGAAGGCTTTTACTGTTGCTCTCAACTTACTCAACA 36
Qy      1389 TGAGAGATTCATACCGGGGTGAACCTT 1417
Db      35 TCAAAATTTCACTTGGCGAGAAACTCT 7

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RESULT 10
US-10-750-623-56682/c
; Sequence 56682, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: NM11100-1
; CURRENT APPLICATION NUMBER: US/10/750, 623
; PRIORITY FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482

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; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 56682
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Bovine 19866880596109
US-10-750-623-56682

Query Match      20.5%; Score 413.8; DB 7; Length 934;
Best Local Similarity 68.0%; Pred. No. 1.9e-121;
Matches 591; Conservative 0; Mismatches 277; Indels 1; Gaps 1;

Qy      550 CATCAGAGACATCATTAAGAGAAATTCCTTGAATGTAAAGACTGTGGAGGCTTTTACT 609
Db      875 CAGAAATTCATCATAGTGTGAACCTTATATCTGAAGAAATGTGAAGAGGCTTTTGT 816
Qy      610 CGTGTCTCAACTTAAGTCAATCAGAAATTCATCTGTGTGAAGAAACCTTATGAATGT 669
Db      815 CATCATTCAGTCTCTATCAACCAAGAAATTCATCTGTGTGAAGAAACCATTAATATGT 756
Qy      670 AAAGAAATGAAGAGGCTTCCTTGGGCAATCAGCTTACTCAACATCAAAAATTCAT 729
Db      755 AAACAGTGTGAAGAGGCTTTTGTTTACAGCTATCTAATCACTGAACATCAGAGAACTCAT 696
Qy      730 ACTGGGAGAGGCTTCAAGATGTAAAGCTGTGGAGAGGCTTTTGCATGGGCTTCAAG 789
Db      695 ACTGGTGAAGAGGCTTCATGATGTAAAGATGTGAAGAGGCTTTTGTAGGGCTTCAAGC 636
Qy      790 CTCGTATTCATTAAGAGATTCATCTGTGAAAAACCTTAAGAAATGTAAAGCTGTGA 849
Db      635 CTTCCTTAAGCATTAAGAGATTCGTAGTGTGAAGAAACCTTAAGATGTGAAGATGTGG 576
Qy      850 AAGGCTTTTCGGGCTGTGTATGATCACTCAGACACAGAAATTCACACTGGGAGAA 909
Db      575 AAGGCTTTCTGTAGATTTATCAATTTACAAACATCAGAAATTCATCTGTGTGAAG 516
Qy      910 GAATCAAGATGCAAGAACTGTGGAGAACTTTAGCCGTGTATTAACCTTATTCAGAC 969
Db      515 CCCATGAATGTAAAGATGTGGAGAACTTTTAAAGCTCAATTCCTTATTAACAT 456
Qy      970 AAGAGATTCATAGTGTGGAGAAAGCTTACAGATGTAAAGACTGTGGAGAGGCTTTTAT 1029
Db      455 CAGATCAATTCACAGTACTTGAACCATATGAATGTAAACATGTGGAGAGGCTTCAAT 396
Qy      1030 TGTGTTTCAAGCCTCATTCAGCATTAAGAAATTCACACAGTGAAGAAACCTTATGAATGT 1089
Db      395 CGTGTGGGAGAACTTTAAATGCATGATCAATTCATCTGGGAGAAACCTTATGAATGT 336
Qy      1090 CAAGAAATGTGGAGAGGCTTTTACTCGATCAATTAACCTTACTCAGCATCAAGAAATCCAC 1149
Db      335 AAGGAATGTGAAGAAACCTTTAAGCTTAATTTCTAAATATATCATCAGCAGATCCAT 276
Qy      1150 ACCGTGAGAAAGCTTCAGAAATGTAAAGATGTGGAGAGGCTTTTGGCTGGGTTGAGC 1209
Db      275 ACTGGCTTGAACCATATATATGTAAAGATGTAAAGAGGCTTTCCGTCTATATACAGT 216
Qy      1210 CTCGTTAAGCAGAGAGATACATACGGGCG-AGAAAGCGTACAGAGACAGAAATGTGG 1268
Db      215 CTTCCTCAACATTAAGAAATTCATCTGTGAAAAAACCTTTATGATGTAAAGAAATGTGG 156
Qy      1269 GAAGGCTTCAATTTGTGCTATCACTCACTCAGACAGAGAAATCCACAGGCGAAAC 1328
Db      155 TAAGGCTTTAATCGTAGCGAGGACTTATTCAGCATCAGAAATTCATATCTGCGTGA 96
Qy      1329 CCGGTATTAATGTAAAGAGTGTGGAGAGGCTTTCACTTATGATTCAGGCTCGTGAACA 1388
Db      95 GCCACATTAATGTACGAAATGCGGGAAGGCTTTTACTGTTGCTCTCAACTTACTCAACA 36
Qy      1389 TGAGAGATTCATACCGGGGTGAACCTT 1417
Db      35 TCAAAATTTCACTTGGCGAGAAACTCT 7

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RESULT 11
US-11-000-688-1136
; Sequence 1136, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUJIGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1136
; LENGTH: 2435
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc feature
; LOCATION: (1)..(2435)
; OTHER INFORMATION: zinc finger protein 354a(ZNF354A) gene.
US-11-000-688-1136

Query Match      20.2%; Score 407.2; DB 8; Length 2435;
Best Local Similarity 61.7%; Pred. No. 4.6e-119;
Matches 649; Conservative 0; Mismatches 403; Indels 0; Gaps 0;

536 CCCCTCTAGAACACATCATGAGACATTAAGAGAAATTCCTTGAATGTAAAGACTGTG 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      CCCTTCGTAAACATGAGAAAAACATATGAGAGAAACTATTAAAGTAAAGATGTT 894
QY      GGAAGGCTTGTGTGTGCTATCAACTTGAATCAATCAAGAAATCCATCTGCTGAGA 655
Db      CAAAAGCTTTAGCCAAAGTTCAAGCTCTTATTCACATCAATTAACATCTGAGAGA 954
QY      AACCTTGAATGTAAAGATGTAAAGAGGCGCTTCGTTGGGGCANTACCTTACTCAAC 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      AACCTTCAATGTAAAGATGTGGAAGCGCTTACTCTCACTGATCAATCCCTTTTAAAC 1014
QY      ATCAAAAAATTCATACGCGGAGAAAGCCCTACGAATGTAAAGACTGTGGGAGGCTTTTC 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      ATCTAAGAACCATATCTGTGAGGAATCTCTACAGATGTAAAGATGTGTTAAATCCTTCA 1074
QY      GATGGGGCTCAAGGCTTCGTATTCATTAAGAGATTCATCTGCTGAAAAACCTTATGAT 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      GCCGAAGGTCAAGGCTTTTATATCATCAAAAAATTCATGCTGAAGAAAAACCTTGTAAGT 1134
QY      GTAAGACTGTGGAAGGCGCTTCGCGGCGTGTAGAGTCACTGACAGCCAGAGATTCC 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      ATATCCGGGTATGGAAGGATTAAGTTCAGACATCCCTTTCTGAGATGTAAGAAATTC 1194
QY      ACACTGGGAGAAAGACTACGAATGCAAGACTGTGGAAGACTTTAGCCCTGTGTATA 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      ATCTAAGAAAGAGCTTACTATGTAAATGATGTGGCAACCTTTAAGTACTACTCAT 1254
QY      AACTTATTCAGCAAGAGAAATTCATAGTGGGAGAGGCTTTACGAGTGTAAAGACTGTG 1015
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      CCTTCGTATCATGAGAAATTCACACTGAGAGAAAGCTTTTAAATGTATGATGTG 1314
QY      GGAAGGCTTTTATTTGTGTTCAAGCTCATTCACAGATTAAGAAATTCACAGAGTGA 1075
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      GGAAGGCTTTCAGCAAGAGTGCCTCTTATTCACATGAAGAAATTCACACGGAAGAA 1374
QY      AACCTTATGATGTCAAGAAATGTGGAGAGGCTTTTACTGAGTCAATTAACCTTACTCAGC 1135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      AGCCCTATGATGATGATGATGTGGAGAAAGCTTTTACTTCTATTCACGACTTAATAGAC 1434
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QY      ATCAAGATCCACACCGGTGAGAAAGCCTCAAGATGTAAAGATGTGGAGAGCCTTTC 1195
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      ACCGAATCATTCATCTGGAAGAGATTTATTAATGTAAATGTGTAAAGCCTTAA 1494
QY      GCTGGGGTTTCAGGCTTCGTTAAGCAGAGAGATACATACGGGCGAGAGCGTTACAAAT 1255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      GCTCCACTCAACACTTATTTATTCAGAGCAATTCATATGAGAAAAACCATGTAAAT 1554
QY      GCAAGATGTGGGAAGGCTTCATTTGCTATCACTCACTCACTGACAGCAAGAAATTC 1315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      GTAAGATGTGGGAAGAAACCTTCAGACAGAGATTCCTTCAATCAATCAAGAAATGC 1614
QY      ACACAGCGAAACCCCGATTAATGTAAAGATGTGGAGAGGCTTCAATTAATGATGCA 1375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      ATACTGAGAAAGACCTTATTAATGTAAAGATGTGGAGAAACATTCAGGTAACTCAT 1674
QY      GCTCGTGAACATGAGAGAAATTCATACCGGGGTGAAAACCTATGGGTGTACAGAAATGTG 1435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      CACTTATGATACACAGAGAAATTCATCTGAGAGAAACCATATGATGTGAGAAATGTG 1734
QY      GGAAGGCTTTAGTACCGGCAATCACTTACACATCAAGAAAAACGACAGTGGGCGCA 1495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      GGATATCTTTTGGCCAAAGTTCAAGCTCTTATTCAGCATCGAAGATTCATACAGAGAAA 1794
QY      AATCCTACGAATGTAAAGAGTGGGGAAGGATGTAAACCATCAATCCGAGAAC 1555
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      AACCTTTAAATGTATATCATGTGAGAAACCTTTTGAACAAAGCTCATCATCATATTGCA 1854
QY      ATCAGAGATCCACAAACAGTTGAAGAGCCTTT 1587
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      ATCAGAGAAATTCATCTGAGAGAAACCTTAT 1886

RESULT 12
US-11-000-688-1179
; Sequence 1179, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUJIGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1179
; LENGTH: 2603
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc feature
; LOCATION: (1)..(2603)
; OTHER INFORMATION: zinc finger protein 3 (zf-51) (ZNF3) gene.
US-11-000-688-1179

Query Match      20.0%; Score 402; DB 8; Length 2603;
Best Local Similarity 60.4%; Pred. No. 2.2e-117;
Matches 737; Conservative 0; Mismatches 470; Indels 13; Gaps 4;

181 AAAACAATGAGCCAGAGGTTTGTGACGTTCCCGCAGTACATGACTTTTCTCAGAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      AAGCCCAAGTCCAGAGACTGTAACTTTGAGATGTAGTGTATCTTATCCGAAG 459
QY      GAGTGGGCTGTCTGAATCTGTCTGAGAGGAGCTGTACTGAGAGTATGTGTGAGAAC 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      GAGTGAAGGCTTTGGAACCTGCTCAGAGGAGCCTTATAGAGATGATGTCTGAGAAAT 519
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QY 301 TACAGTAAGTGGTCTCACTGATTTGAGTCAGCATATGAAATTAAGATTACTTACA 360
DB 520 TACGGAAATGTGTCTCATCTGATCGTAGACGAGACTGAAATATGATCAAGAAATTTCT 579
QY 361 GAAAAAACATTCATGAATTAAGGCTTCCAAAAGAAATTCAGATGAAGAAATTAATCC 420
DB 580 GAAAGCA----CAAGATCAATGGGCTCTACTGGA--AGATTCAAAAGGATATTT 631
QY 421 CTTCGCGCTGATGTATGTGAAGGTACGCTTGAAGACCAAGCGCTCCAGAGGAG 480
DB 632 CTCAGGCTCAAGTTTAAAGAAAGCTTAAGAACGAAGATCACTGAAAAGCGCGTGG 691
QY 481 TATGTCAATCAATGATCATCAATTATGTCAAAAGCGCTGTACTAGAGAGGCACTT 540
DB 692 GGAATCCCTCCGAGAGAAAGCTGAACAGGAAATATGCAATTTTGTCTCAAGTACAGTTG 751
QY 541 CCTAAGACATCAAGAGACATCATTAAGGAATTCCTTGAATGTAAAGACTGTGGAAAG 600
DB 752 AGAGAGAGCTAACCCCGAGGGA---GAGAGAGGAGAGAAATATATATATTTGGGAAC 807
QY 601 GCCTTATGCTGGCTATCACTTAAGTCAACATCAGAAATCCATATCTGTGAGAACT 660
DB 808 AGCTTCACTGTGAATTCACACTTATCTCAGATCAGAGACTCCCGTGGAGAGACAGACC 867
QY 661 TATGAATGTAAAGATGTAAAGAGCGCTTCGTTGGGGAATCACTTACTCAATCA 720
DB 868 CATTAAGTGTAGATGTAGTGAAGAGCTTAAATCGAATTCAGACCTTATTCACATCAG 927
QY 721 AAAATTCATACCTGGGAGAAAGCGCTGATGTAAAGACTGTGGAAAGCTTTGCATGG 780
DB 928 AGAATTCACCTGGGAAAGCGCTTATGAATGTAAAGTGTGGAAAGCGCTTCAAGCAG 987
QY 781 GGTCAAGCGCTGTATTCATTAAGAGATTCATATCTGTGAAAAAAGCTTATGATTA 840
DB 988 AGCTCACACTTATTCAGATTCAGAAATCCACACTGGGAAAAAAGCTTATGATTA 1047
QY 841 GACTGTGAAAGCGCTTGGCGGTGTATGATGAGCTCACTCAGACAGAGATTCACACT 900
DB 1048 GATTTGGGAAAAAGCTTCAAGCTGTAGCTCGCCCTATCTGTGATCGAGGATCCACAG 1107
QY 901 GGGGAAAGAGCTGAGATGCAAGAGCTGTGGGAAAGCGCTTACCGTGTGTAACTT 960
DB 1108 GGGGAAAGAGCTTATGAATGTATGTAGTGTGGAAAGCGCTTCAAGCTGAGCTCACCTC 1167
QY 961 ATTCAAGCAAGAGATTCATATGTGGGAGAGCGCTTACAGATGTAAAGCTGTGGAAAG 1020
DB 1168 ACCCACTCAAGAGATTCACACTGTGTGAGAAAGCTTACGCTGTGATGTATGTGGAAAG 1227
QY 1021 GCTTTATTTGTGTCAAGCGCTCATTCAGCATTAAGAAATTCACAGGTGAGAAAGCC 1080
DB 1228 GCCTTCAGCAGAGAGCTCAACCTTATTCACATCAGAGATTCACACTGGAGAAAAAGCC 1287
QY 1081 TATGAATGTCAAGATGTGGAAAGCGCTTACTGAGTCAATTAAGCTTACTGAGATCAG 1140
DB 1288 TATGAATGTATGAATGTGGAAAGCGCTTCAAGCAGAGCTCACACCTTATTCAGACAG 1347
QY 1141 AAGATCAAGAGCGGTGAGAAAGCGCTCAAGATGTAAAGAGTGTGGAAAGCGCTTCCCTGG 1200
DB 1348 AGAATCAAGCTGTGAGAGAGAGCGCTTACAGATGTATGTGAATGTGAGAGAAAGTTACTTAC 1407
QY 1201 GGTTCAGAGCTGTTAAGCAGAGAGATCATACGGGCGAGAAAGCGGTCAAGTGCACA 1260
DB 1408 AGTTCAAGCGCTTATTCAGATCAAGAAATTCACACCGGAGAGAAAGCCCTTATGATTAAGT 1467
QY 1261 GAATGTGAGAAAGCGCTTCAATTTGTGCTATCACTCACTAGACAGAGAAATTCACACA 1320
DB 1468 GAGTGTGAGAAAGCGCTTCAAGTACAGCTCGCTTGTGTGCGATCAGAAATTCACACT 1527
QY 1321 GGGGAAAGCGCTTATTAATGTAAAGAGTGTGGAAAGCGCTTCAATTAAGATGAGAGCTC 1380
DB 1528 GAGAGAGAGCGCTTATTAATGTGAGATGTGAGATGAGAGAAAGCTCCCTCAGAGTTACAGCCGA 1586
QY 1381 GTGAAACATGTAGAAATTCAC 1400

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DB 1587 GTTAAATATCAGAGAGTCCA 1606

RESULT 13
US-11-136-527-3206
; Sequence 3206, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 3206
; LENGTH: 3350
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3206

Query Match 19.9%; Score 401.4; DB 8; Length 3350;
Best Local Similarity 61.8%; Pred. No. 4.1e-117;
Matches 624; Conservative 7; Mismatches 378; Indels 0; Gaps 0;

QY 564 TAAAGAAATTCCTTGAATGTAAAGAGCTGTGGAAAGCGCTTATGCTGTGCTATCAACT 623
DB 1215 TGAAGAGAAAGCGCTTGAATGTAAAGTGTAGTGTGCAAGTCTTCACTGAGCTCCCATCT 1274
QY 624 TAGTCAACATCAGAAATCCATCTAGTGTGAGAAAGCTTATGATGTAAAGATGTAAAGA 683
DB 1275 CATTTGCTACCAAGAACCCATACGGGGGAAAGCGGTACAAATGCAACTGTGTGGGAA 1334
QY 684 GGCCTTCGTTGGGCAATCACTTACTCAATCAATCAAAATTCATCTGGGAGAGAGCC 743
DB 1335 GTTCTTCAACCGGAGGTCAAGTGTCTCATCAGAGAGATTCATCTGAGAGAGAAAGCC 1394
QY 744 CTACGAATGTAAAGAGCTGTGGAAAGCGCTTGTGATGGGCTCAAGCTGTGATTCATTA 803
DB 1395 ATACAGGTGCAATCTGTGTGGAAAGCTTTCACCAAGATGTGTCTGTGTGTATCA 1454
QY 804 GAGGATTCATCTGTGAAAGAAAGCGCTTATGATGTAAAGAGCTGTGAAAGCGCTTGTGGCG 863
DB 1455 AAGAACTCACTGGGAGCGCTTATGATGTGAATGCAACAGTGTGGAGTCTGTCCGCCA 1514
QY 864 TGTGTATGAGCTCACTCAGACACAGAGATTCACACTGTGGGAGAAAGACTACGAATGCAA 923
DB 1515 GAGCTTCAAAAGCTCATTTGGCGCATCAAGAACCCACAGAGAAAGCGGTACGAATGCAC 1574
QY 924 AGACTGTGGGAAAGCGCTTATGAGCGGTGTATTAAGTTATTCAGCACAAGAAATTCATAG 983
DB 1575 CCAAGTGTGGAAAGCTCATTCATCAGATGTAAAGAGCTTCAAGCTCAAGCAAAAATTCATCTC 1634
QY 984 TGGGAGAAAGCGCTTCAAGTGTAAAGAGCTGTGGAAAGCGCTTATTTATTTGTGTCAAGCT 1043
DB 1635 TGGAGAAAGCGCTTATGATGTGAGTCACTGTGTGCAAGTCTTCAAGCAAGCTTATTAAGCT 1694
QY 1044 CATTCAGATTAAGAAATTCACACAGGTGAGAAAGCGCTTATGATGTCAAGAAATGTGGAA 1103
DB 1695 TGTGTCCATTCAGAGAGCTCAACAKAGAGAAAGCGCTTCAAGTGTATCTAGTGTGGAA 1754
QY 1104 GGCCTTATCTCAGATCAATTAAGCTTACTCAGATCAAGAAATTCACACCGGTGAGAGGCC 1163
DB 1755 ATCAATTCAGCTGAGCTCMACAGCTGTGTCTCATCAAAAGAAAGCCACAGCGKAGAGAGCC 1814
QY 1164 TCACGAATGTAAAGAGTGTGGAAAGCGCTTGTGCTGGGCTTGTGAGCTGTGTAAGCAGCA 1223
DB 1815 TTACKATGTAAAGAGTGTGGAAATCATTCATCAATGAGAGCTCACACTTGTATGACCA 1874

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US-10-750-185-30010

Query Match 19.3%; Score 388.8; DB 7; Length 1330;
Best Local Similarity 62.0%; Pred. No. 2.3e-113;
Matches 615; Conservative 0; Mismatches 377; Indels 0; Gaps 0;

Search completed: February 6, 2006, 22:13:57
Job time : 399 secs

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OY 566 AGAGAAATTCCTTTGAAATGAAGACTGTGGGAAGCCCTTATGTCGTGCTATCACTTA 625
DB 992 AAGAGAAATGTCATAAATGTGAAGATGTGAAGGTTTTGTCCGCAAGGCTCATTTCA 933
OY 626 GTCAACATCAAAAATCCATCTGTGTGAAGAACCTTATGAATGTAAAGATGTAGAAG 685
DB 933 TTCAACATCAAAAGGCTCATCTGAGAGAAACCTTCCAAATGTAAATGTGGAAAA 873
OY 686 CCTCCGTTGGGGCATCACTTACTCAATCAAAAAATTCACTAGGGGAGAAAGCCCT 745
DB 872 GTTTTAGTCGAGTTTATTTGTTAATGAAATCAGAAATTCACACCGGGAAAGCCCT 813
OY 746 ACGAATGTAAAGACTGTGGGAAGCTTTTGCATGGGCTCAAGCCTCGTTATTCATPAGA 805
DB 812 ATGAGGTAAATATTGCGGAAAAACCTTTAGTGTGAGCTCAACCTTATTAGCATCAGA 753
OY 806 GGATTCTACTGTGTAAAAACCTATGAATGTAAAGACTGTGAAAGCCCTTCGGCGTG 865
DB 752 GAATCCACACTGGAGAGAGACCTATCAGTGTATCATGTAAACAGAGCTTCAGCCAGC 693
OY 866 GTGATGAGCTCACTGAGCAACAGAAATTCACACTGGGGGAAAGACTAGCAAG 925
DB 692 GAAAGAACCTTGTAAACATCAGAGATTCACAGGTGAAACCCCATAAATGTAGTG 633
OY 926 ACTGTGGGAAGACCTTTAGCCGTGTATTAACCTTATTCAGCACAAGAGATTCATAGTG 985
DB 632 ACTGTGGGAAGCTTTCAGTTGGAAGTCAACCTGATTTGAACATCAGAGAACACACTG 573
OY 986 GGGAGAACCTTACGAGTGTAAAGACTGTGGGAAGCCCTTATTTGTGTTCAAGCTCA 1045
DB 572 GTGAGAAACCTATCTGTACCTGTACCAATGTAAAGACTTATGTAGAAATTCCTTACTTG 513
OY 1046 TTCAGCATAAAGAAATTCACACAGGTGAGAAACCTATGAATGTCAAGAAATGTGGAAAG 1105
DB 512 TTGAACATCAGAAATTCACACTGGGAAAGACCCCATAAATGTGTGAATGTGGAAAG 453
OY 1106 CCTTTACTGAGTCAATTAACCTTACTCAGCATCAGAAATCCACCGGTGAGAGCCTC 1165
DB 452 CCTTTAGATTAAATACATATCTTATCAACACCAAAAAATCCACCTGTGAGAAACCTT 393
OY 1166 ACGAATGTAAAGAGTGTGGGAAGCCCTTGTGGGCTTCAGCCTTCGTTAAGCAGAGA 1225
DB 392 TTCTTTGTATGTGAATGTGAAAAAGCTTCAGTGGAGCTCATTCCTTATTTGAACATCAGA 333
OY 1226 GGATACATACGGGCGAAGACCGTAACAGTGCACAGAAATGTGGGAAGGCTTCATTTGTG 1285
DB 332 GAATCCATACAGGTGAAAGACCTTATCAGTGCAAAGAGTGTGGAAAAAGCTTCAGTCAAC 273
OY 1286 GCTATCACTCACTCAGCAGAGAGAAATCCACAAGGCGAAACCCGTTATTAATGTAAAG 1345
DB 272 TTTCGAACCTTACTCGCATCAGGAATTCACAAGGGGCAAAACCCCATAAATGTGAGG 213
OY 1346 AGTGTGGAAAGCTTTTCAATTATGATCGAGCTCGTGAACATGAGGAATTCATACCG 1405
DB 212 AATGTGAAAAAGCCTTTAGTGAAGCTCAGGTCTTATTCAGCACAGAGAAATCCACACCA 153
OY 1406 GGGTGAACCTTANGGGTGTACAGAAATGTGGGAAGGCTTATGTCACGGCCATCAGCTTA 1465
DB 152 GAGAGAAAGATTATTCATACATGAAGAACAAAGAAAGTTTGAACCAATGAGAGCTTTG 93
OY 1466 CACAAATCAGAAAACGCAAGTGGGCGAAATCTTACGAATGTAAAGAGTGGCGGAAG 1525
DB 92 TTATACAGAGAGAGTACCTAACCTTAAGSAAAAATCTTATAATGTGAATGTGGAAAA 33
OY 1526 CATGTAAACCACTTAACCATCTCGAGAACAT 1557
DB 32 CTTTCAGTGTCAGTGCTCATCTTGTGCACAT 1
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OM nucleic - nucleic search, using sw model

Run on: February 6, 2006, 21:33:22 ; Search time 1666 Seconds
(without alignments)
10001.679 Million cell updates/sec

Title: US-10-111-257-3

Perfect score: 2015
Sequence: 1 cgccttcgcaccggtgacgc.....gtgaagttcccaacttaa 2015

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1967.4	97.6	2173	7	US-10-221-625-108 Sequence 108, App
2	1946.2	96.6	3293	3	US-09-764-864-123 Sequence 123, App
3	1420.2	70.5	1453	7	US-10-296-115-424 Sequence 424, App
4	1397.8	69.4	1429	7	US-10-641-643-689 Sequence 689, App
5	734.6	36.5	4483	9	US-10-499-353A-332 Sequence 332, App
6	703	34.9	2143	3	US-09-881-578-3 Sequence 3, Appl1
7	703	34.9	2143	3	US-10-623-914-3 Sequence 3, Appl1
8	618	30.7	1945	6	US-10-094-749-1120 Sequence 1120, Ap
9	615.4	30.5	2235	6	US-10-108-260A-2359 Sequence 2359, Ap
10	603.6	30.0	1900	3	US-10-450-763-25299 Sequence 25299, A
11	593.6	29.5	774	3	US-09-764-864-567 Sequence 567, App
12	584.4	29.0	592	6	US-10-029-386-13162 Sequence 13162, A
13	546	27.1	3163	9	US-10-786-148-116 Sequence 116, App
14	538.6	26.7	1813	7	US-10-121-625-162 Sequence 162, App
15	538	26.7	4683	6	US-10-094-749-1085 Sequence 1085, Ap
16	538	26.7	4683	6	US-10-450-763-5630 Sequence 5630, Ap
17	520.6	25.8	2274	5	US-10-037-270-154 Sequence 154, App
18	520.6	25.8	2274	6	US-10-117-722-154 Sequence 154, App
19	520.6	25.8	2274	6	US-10-122-851-154 Sequence 154, App
20	510.2	25.3	526	3	US-09-954-531-545 Sequence 545, App
21	510.2	25.3	526	3	US-10-843-641A-1612 Sequence 1612, Ap
22	510	25.3	2499	6	US-10-120-988-331 Sequence 331, App
23	506.6	25.1	4216	9	US-10-450-763-12507 Sequence 12507, A

24	506.6	25.1	6907	9	US-10-450-763-3997 Sequence 3997, Ap
25	503.4	25.0	1635	3	US-09-864-761-16962 Sequence 16962, A
26	502.8	25.0	2075	5	US-10-098-841-110 Sequence 110, App
27	502.8	25.0	3472	6	US-10-104-047-415 Sequence 415, App
28	500.8	24.9	1931	6	US-10-108-260A-113 Sequence 113, App
29	500.8	24.9	2521	6	US-10-094-749-1398 Sequence 1398, Ap
30	499	24.8	2266	6	US-10-094-749-418 Sequence 418, App
31	495.6	24.6	1268	6	US-10-029-386-25225 Sequence 25225, A
32	495.4	24.6	1694	6	US-10-104-047-1500 Sequence 1500, Ap
33	489.6	24.3	1907	7	US-10-121-625-142 Sequence 142, App
34	488.8	24.3	3139	5	US-10-198-846-13470 Sequence 13470, A
35	488.2	24.2	990	3	US-09-864-761-26905 Sequence 26905, A
36	486.8	24.2	1919	3	US-09-864-761-10504 Sequence 10504, A
37	486	24.1	4797	5	US-10-171-311-231 Sequence 231, App
38	486	24.1	4797	8	US-10-645-756-43 Sequence 43, Appl1
39	483.8	24.0	1716	6	US-10-029-386-24986 Sequence 24986, A
40	478.2	23.7	2925	5	US-10-037-270-163 Sequence 163, App
41	478.2	23.7	2925	6	US-10-117-722-163 Sequence 163, App
42	478.2	23.7	2925	9	US-10-122-851-163 Sequence 163, App
43	474.8	23.6	2241	6	US-10-104-047-693 Sequence 693, App
44	473.2	23.5	5830	6	US-10-242-355-960 Sequence 960, App
45	464.4	23.0	4132	5	US-10-198-846-13133 Sequence 13133, A

ALIGNMENTS

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RESULT 1
US-10-221-625-108
; Sequence 108, Application US/10221625
; Publication No. US2004003942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dyrng Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221,625
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 108
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2004003942A1 095210CB1
US-10-221-625-108

Query Match          97.6%; Score 1967.4; DB 7; Length 2173;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 QY 1089 GGTGTATTAACCTTATTCAGCAACAAGAAATTCATATGTTGGGAGAGGCTTTAGAGTGA 1148
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RESULT 2

US-09-764-864-123
 ; Sequence 123, Application US/09764864
 ; Patent No. US20020132753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT223
 ; CURRENT APPLICATION NUMBER: US/09/764,864
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1792
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 123
 ; LENGTH: 3293
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-764-864-123

Query Match 96.6%; Score 1946.2; DB 3; Length 3293;
 Best Local Similarity 98.3%; Pired. No. 0;

Matches 2010; Conservative 0; Mismatches 3; Indels 32; Gaps 3;

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Db 138 AGTGAAGAAACCGACACTGTGTAGCTCTAGCCTCTCGGAATTTGTCTTCTTCACTAGTGAAC 197
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QY 991 AAGCCTTACGAGTGTAAAGACTGTGGGAAAGGCTTTTATTTGTGTTCAAGCCTCATTCAG 1050
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QY 1111 ACTGAGTCAATTACCTTACTCAGATCAGAAAGATCCACCCGTGAGAAAGCCTTACGAA 1170
Db 1156 ACTGAGTCAATTACCTTACTCAGATCAGAAAGATCCACCCGTGAGAAAGCCTTACGAA 1215
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QY 1891 AGTCTCACTTTGCTTAAACGTGCCCAAGAGAGAGATGATGCTGTGATTCGG 1950
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QY 2011 TTAAG 2015
Db 2056 TTAAG 2060
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RESULT 3
US-10-296-115-424/c
; Sequence 424, Application us/10296115

Publication No. US20040053248A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq Inc
 TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
 FILE REFERENCE: 784CT
 CURRENT APPLICATION NUMBER: US/10/296,115
 CURRENT FILING DATE: 2002-11-18
 PRIOR APPLICATION NUMBER: US09/488,725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US09/552,317
 PRIOR FILING DATE: 2000-04-25
 NUMBER OF SEQ ID NOS: 1478
 SEQ ID NO 424
 LENGTH: 1453
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-296-115-424

Query Match 70.5%; Score 1420.2; DB 7; Length 1453;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1446; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

QY 567 GGAGAAATTCCTTGAATGTAAAGACGTGTGGAAAGCCTTTAGTCGTGGCTATCACTTGA 626
 DB 1453 GGAGAAATTCCTTGAATGTAAAGACGTGTGGAAAGCCTTTAGTCGTGGCTATCACTTGA 1394
 QY 627 TCAACATCAGAAAAATCCATCTACTGTGAGAAACCTTATGAAATGTAAAGAAAGGC 686
 DB 1393 TCAACATCAGAAAAATCCATCTACTGTGAGAAACCTTATGAAATGTAAAGAAAGGC 1334
 QY 687 CTTCCTGTGGGCAATCACTTACTCAACATCAAAAAATTCATATCTGGGAGAAAGCCTTA 746
 DB 1333 CTTCCTGTGGGCAATCACTTACTCAACATCAAAAAATTCATATCTGGGAGAAAGCCTTA 1274
 QY 747 CGAAATGTAAAGACGTGTGGAAAGCCTTTGATGTGGGCTCAAGCCTGTTATTAAGAG 806
 DB 1273 CGAAATGTAAAGACGTGTGGAAAGCCTTTGATGTGGGCTCAAGCCTGTTATTAAGAG 1214
 QY 807 GATTCTACTGTGTGAAGAAACCTTATGAAATGTAAAGACGTGTGAAGAAAGCCTTTGCGGCTG 866
 DB 1213 GATTCTACTGTGTGAAGAAACCTTATGAAATGTAAAGACGTGTGAAGAAAGCCTTTGCGGCTG 1154
 QY 867 TGAATGACTCACTCAGACCAAGAAATTCACACTGTGGAGAAAGAACTTACGAATGCAAG 926
 DB 1153 TGAATGACTCACTCAGACCAAGAAATTCACACTGTGGAGAAAGAACTTACGAATGCAAG 1094
 QY 927 CTGTGGAAAGCCTTTAGCCGTGTATTAACCTTATTCAGACCAAGAAATTCATAGTGG 986
 DB 1093 CTGTGGAAAGCCTTTAGCCGTGTATTAACCTTATTCAGACCAAGAAATTCATAGTGG 1034
 QY 987 GGAGAAAGCCTTACGAGTGTAAAGACGTGTGGAAAGCCTTTATTTGTGTCAAGCCTCAT 1046
 DB 1033 GGAGAAAGCCTTACGAGTGTAAAGACGTGTGGAAAGCCTTTATTTGTGTCAAGCCTCAT 974
 QY 1047 TCAGCATAAAGAAATTCACACAGGTGAGAAACCTTATGAATGTCAAGAAATGTGGAAAGC 1106
 DB 973 TCAGCATAAAGAAATTCACACAGGTGAGAAACCTTATGAATGTCAAGAAATGTGGAAAGC 914
 QY 1107 CTTTACTCGAGTCAATTAACCTTACTCAGCATCAAGAAATTCACACCGGTGAGAAAGCCTCA 1166
 DB 913 CTTTACTCGAGTCAATTAACCTTACTCAGCATCAAGAAATTCACACCGGTGAGAAAGCCTCA 854
 QY 1167 CGAATGTAAAGAGTGTGGAAAGCCTTTGCTGTGGGCTTCAGCCTCGTTAAGACAGAG 1226
 DB 853 CGAATGTAAAGAGTGTGGAAAGCCTTTGCTGTGGGCTTCAGCCTCGTTAAGACAGAG 794
 QY 1227 GATACATACGCGGAGAAAGCCTTACAAAGTGCACAGAAATGTGGAAAGCCTTCAATTGTGG 1286
 DB 793 GATACATACGCGGAGAAAGCCTTACAAAGTGCACAGAAATGTGGAAAGCCTTCAATTGTGG 724
 QY 1287 CTATCACTTCACTCAGACCAAGAAATTCACACAGGGAAACCCCGTATTAAGTAAAG 1346
 DB 733 CTATCACTTCACTCAGACCAAGAAATTCACACAGGGAAACCCCGTATTAAGTAAAG 674

QY 1347 GTGTGGAAAGCCTTCAATTAATGATCGAGCCTCGTGAACATGAGAAATTCATACCGG 1406
 DB 673 GTGTGGAAAGCCTTCAATTAATGATCGAGCCTCGTGAACATGAGAAATTCATACCGG 614
 QY 1407 GGTGAAACCTTATGGGTGTACGAATGTGGAAAGCCTTTAGTCACGCGCATCAGCTTAC 1466
 DB 613 GGTGAAACCTTATGGGTGTACGAATGTGGAAAGCCTTTAGTCACGCGCATCAGCTTAC 554
 QY 1467 ACAACATCAGAAAAAGCAGAGGGGCGAAATCTACGAATGTAAAGAGTGGCGGAAAGC 1526
 DB 553 ACAACATCAGAAAAAGCAGAGGGGCGAAATCTACGAATGTAAAGAGTGGCGGAAAGC 494
 QY 1527 ATGTAAACGACCTTAAACATCTCCGAGAACATGAGAGATCCAAACAGTTGAAGACCTT 1586
 DB 493 ATGTAAACGACCTTAAACATCTCCGAGAACATGAGAGATCCAAACAGTTGAAGACCTT 434
 QY 1587 TTGAACGAGTACCCCGCTCGTATCTATGTGTTGCTTCCACAGTTTGTACCTGCAAT 1646
 DB 433 TTGAACGAGTACCCCGCTCGTATCTATGTGTTGCTTCCACAGTTTGTACCTGCAAT 374
 QY 1647 CAACGACGTTCAAAAAATTAATGAAAAATTCAGAAATTAAGAAATTTAAGTCTCAA 1706
 DB 373 CAACGACGTTCAAAAAATTAATGAAAAATTCAGAAATTAAGAAATTTAAGTCTCAA 314
 QY 1707 ATGTGTGCTCTTGTGAGTACGCTGATGAATCTCTGCTGCTCCGCTCCAGCCGCGG 1766
 DB 314 ATGTGTGCTCTTGTGAGTACGCTGATGAATCTCTGCTGCTCCGCTCCAGCCGCGG 254
 QY 1767 GGAATGAGTCAATCCCTTGTGTGACAGACATCCACGCTGTATACGCCACCCACCTGCTAG 1826
 DB 253 GGAATGAGTCAATCCCTTGTGTGACAGACATCCACGCTGTATACGCCACCCACCTGCTAG 194
 QY 1827 TGACCTTAGTACGCTTGTGTATGATCAGATCAATCCAGCA--TGACAGTCCCTGTG 1885
 DB 193 TGACCTTAGTACGCTTGTGTATGATCAGATCAATCCAGCAATTCACAGATTCACAGTCTGTGAC 134
 QY 1886 CAAGTAGTCTCACTTGTCTTAAACAGTGGCCCAAGAGACAGAGTAG--TGATCTGG 1942
 DB 133 CAAGTAGTCTCACTTGTCTTAAACAGTGGCCCAAGAGACAGAGTAGATGATCTGG 74
 QY 1943 TGATTTGGAATATGCCAAAGAAAGCCAAAGTGTCTCTTTTAAATGAAAAAGTGAAG 2002
 DB 73 TGATTTGGAATATGCCAAAGAAAGCCAAAGTGTCTCTTTTAAATGAAAAAGTGAAG 14
 QY 2003 TTCTCACTTAA 2015
 DB 13 TTCTCACTTAA 1

RESULT 4
 US-10-641-643-689
 ; Sequence 689, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 APPLICANT: Cocks, Benjamin G.
 Susan G. Stuart
 Jeffrey J. Selhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 GENE EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 689:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TLYMNOT02
CLONE: 450088
SEQUENCE DESCRIPTION: SEQ ID NO: 689 :
US-10-641-643-689

Query Match      69.4%; Score 1397.8; DB 7; Length 1429;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1411, Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 555 GGGAGGCGCTTAAGTCGAGGCTATCACTTAACAATCAAGAAATCCATCTGTGTG 654
DB 10 GGGAGGCGCTTAAGTCGAGGCTATCACTTAACAATCAAGAAATCCATCTGTGTG 69
QY 655 AAACCTTAAGTAAAGTAAAGTAAAGAGGCTTCCTGGGCAATCAGCTACTCA 714
DB 70 AAACCTTAAGTAAAGTAAAGTAAAGAGGCTTCCTGGGCAATCAGCTACTCA 129
QY 715 CATCAAAAATTCATCTAGTGGGAGAAAGCCCTACGAATGTAAGAAGCTGTGG--AAGGCTT 772
DB 130 CATCAAAAATTCATCTAGTGGGAGAAAGCCCTACGAATGTAAGAAGCTGTGGAGAAAGGCTT 189
QY 773 TTCCGATGGGCTCAAGCCCTGTTATTCATTAAGAGATTTATCTAGTGAAGAAACCTTAAG 832
DB 190 TTCCGATGGGCTCAAGCCCTGTTATTCATTAAGAGATTTATCTAGTGAAGAAACCTTAAG 249
QY 833 AATGTAAGAAGTGTGAAGAGGCTTCCTGGGCTGTGATGAGCTCACTGACACAGAGAT 892
DB 250 AATGTAAGAAGTGTGAAGAGGCTTCCTGGGCTGTGATGAGCTCACTGACACAGAGAT 309
QY 893 TTCACACTGGGGAGAAAGACTACGAATGCAAAAGCTGTGGAGAAAGCTTTAGCCGTGTGT 952
DB 310 TTCACACTGGGGAGAAAGAGNNATGCAATGCAAAAGCTGTGGAGAAAGCTTTAGCCGTGTGT 369
QY 953 AATAAATTATTCAGACACAGAAATTCATAGTGGGAGAAAGCTTACAGGTAAAGACT 1012
DB 370 AATAAATTATTCAGACACAGAAATTCATAGTGGGAGAAAGCTTACAGGTAAAGACT 429
QY 1013 GTGGAGAGGCTTTATTTGTGTGTTCAAGGCTCATTGAGATTAAGAAATTCACAGAGTG 1072
DB 430 GTGGAGAGGCTTTATTTGTGTGTTCAAGGCTCATTGAGATTAAGAAATTCACAGAGTG 489
QY 1073 AGAAACCTTAATGATGTCAGAAATGTGGAGAGGCTTTACTGAGTCAATTACCTTACTC 1132
DB 490 AGAAACCTTAATGATGTCAGAAATGTGGAGAGGCTTTACTGAGTCAATTACCTTACTC 549
QY 1133 AGCATCAGAAAGATTCACACCGGTGAGAGGCTTCAGAAATGTAAGAGTGTGGAGAGGCTT 1192
DB 550 AGCATCAGAAAGATTCACACCGGTGAGAGGCTTCAGAAATGTAAGAGTGTGGAGAGGCTT 609
QY 1193 TTCCGCTGGGGTTCGAGCCTGTTAAGCAGAGAGATTCATACGGGCGAAGAGCGGTACA 1252
DB 610 TTCCGCTGGGGTTCGAGCCTGTTAAGCAGAGAGATTCATACGGGCGAAGAGCGGTACA 669

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QY 1253 AGTGCACAGAAATGTGGAGAAAGGCTTCAATGTGCTATCACTCACTGACAGACAGAGA 1312
DB 670 AGTGCACAGAAATGTGGAGAAAGGCTTCAATGTGCTATCACTCACTGACAGACAGAGA 729
QY 1313 TCACACAGAGCGAAACCCCGTAAATGTAAGAGTGTGGAGAGGCTTCAATTATGAT 1372
DB 730 TCACACAGAGCGAAACCCCGTAAATGTAAGAGTGTGGAGAGGCTTCAATTATGAT 789
QY 1373 CGAGCCTCGTGAACATGAGAGAAATTCATACCGGAGGTGAACCTTAATGGGTACAGAA 1432
DB 790 CGAGCCTCGTGAACATGAGAGAAATTCATACCGGAGGTGAACCTTAATGGGTACAGAA 849
QY 1433 GTGGAGAGGCTTTAGTCAAGGCTCATCGCTTACACACATCAAGAAAGGACAGTGGGG 1492
DB 850 GTGGAGAGGCTTTAGTCAAGGCTCATCGCTTACACACATCAAGAAAGGACAGTGGGG 909
QY 1493 CGAAATCCCTACGAATGTAAGAGTCCGGGAGAGCATGTAAACCACTTAATCCATCCGAG 1552
DB 910 CGAAATCCCTACGAATGTAAGAGTCCGGGAGAGCATGTAAACCACTTAATCCATCCGAG 969
QY 1553 AACATCAGAGATTCACAAACAGTTGAAGAGCCTTTTGAACGAGTAGCCCGCTCGTATCT 1612
DB 970 AACATCAGAGATTCACAAACAGTTGAAGAGCCTTTTGAACGAGTAGCCCGCTCGTATCT 1029
QY 1613 ATGTTTGGCTTTCCACAGTTTGTACTGTCAGTCACTGCGAGTTCAAAAATTTAAATG 1672
DB 1030 ATGTTTGGCTTTCCACAGTTTGTACTGTCAGTCACTGCGAGTTCAAAAATTTAAATG 1089
QY 1673 GAAATTCAGAAATTAAGAAATTTAAGTCAAAATGGTGGCCCTTGAAGTAGGCTGA 1732
DB 1090 GAAATTCAGAAATTAAGAAATTTAAGTCAAAATGGTGGCCCTTGAAGTAGGCTGA 1149
QY 1733 TGAATCTCTGCTGCTCCGCTCCAGCCGCGCGGAGATGTAGTCAATCCCTTGGTCCAGC 1792
DB 1150 TGAATCTCTGCTGCTCCGCTCCAGCCGCGCGGAGATGTAGTCAATCCCTTGGTCCAGC 1209
QY 1793 ACATCCAGCGCTGTATACCCACCCACCTGCTAGTGAAGTAAAGTCCCTTGGTGAATCA 1852
DB 1210 ACATCCAGCGCTGTATACCCACCCACCTGCTAGTGAAGTAAAGTCCCTTGGTGAATCA 1269
QY 1853 GATCAACTATCCACATCAAGTGCCTGTGCCAAGTATGCTCACTTGTGCTTAACAGT 1912
DB 1270 GATCAACTATCCACATCAAGTGCCTGTGCCAAGTATGCTCACTTGTGCTTAACAGT 1329
QY 1913 GGCCCAAGAGCAGAGATGATGATGCTGTGATTCGATATGCCAAGAGAGCCACAA 1972
DB 1330 GGCCCAAGAGCAGAGATGATGATGCTGTGATTCGATATGCCAAGAGAGAGCCACAA 1389
QY 1973 AGTGCTTCTTTTAAATGAAAGGTGAAGTTCGAACTT 2012
DB 1390 AGTGCTTCTTTTAAATGAAAGGTGAAGTTCGAACTT 1429

RESULT 5
US-10-499-353A-332
; Sequence 332, Application US/10499353A
; Publication No. US20050123551A1
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes ar
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 332
; LENGTH: 4483

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TYPE: DNA
ORGANISM: Homo sapien
US-10-499-353A-332

Query Match 36.5%; Score 734.6; DB 9; Length 4483;
Best Local Similarity 91.2%; Pred. No. 2e-215;
Matches 791; Conservative 0; Mismatches 74; Indels 2; Gaps 1;

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QY 47 CAGGCCAGATCCTTCAGAAAAAGCATCCCGAGAGGAAAGCATCGTTAAACATCTT 106
DB 1184 CAGGCCAGATCCTTCAGAAAAAGCATCCCGAGAGGAAAGCATCGTTAAACATCTT 1243
QY 107 AGGTGAGCTCTAGCCTCTCGAATTTGTCTTCTTCAGTGAAGAACCCGAGAACTGATC 166
DB 1244 AGGTGAGCTCTAGCCTCTCGAATTTGTCTTCTTCAGTGAAGAACCCGAGAACTGATC 1303
QY 167 AGTTCCTTCAGTTCTTAAACATATGCCCCAGGGTTTGGTACCTTCCGACCTAGCCATG 226
DB 1304 AGTTCCTTCAGTTCTTAAACATATGCCCCAGGGTTTGGTACCTTCCGACCTAGCCATG 1363
QY 227 ACTTTTCTCAGAGAGAGTGGGCTGTCTGAACTCTGCTCAGAGGAGACTGTACTGGGAG 286
DB 1364 ACTTTTCTCAGAGAGAGTGGGCTGTCTGAACTCTGCTCAGAGGAGACTGTACTGGGAG 1423
QY 287 TGATGCTGAGAACTACAGTAATTTGCTCTCACTGATTTTGAAGTACGATATGAATAA 346
DB 1424 TGATGCTGAGAACTACAGTAATTTGCTCTCACTGATTTTGAAGTACGATATGAATAA 1483
QY 347 AGAGTTTACCTACAGAAAAAACATTCATGAATAAGGGCTTCCAAAGAAATTCAGATA 406
DB 1484 AGAGTTTACCTACAGAAAAAACATTCATGAATAAGGGCTTCCAAAGAAATTCAGATA 1543
QY 407 GAAGAACTAATCCCTTGGCCGTACCTGATGATGTGAAGGATCGTTGAAGACCAAGC 466
DB 1544 GAAGAACTAATCCCTTGGCCGTACCTGATGATGTGAAGGATCGTTGAAGACCAAGC 1603
QY 467 GCTCCAGAGGAGATATGTCAATCAGATGATCATCAATTAATGTCAAAAGCCCTGACTA 526
DB 1604 GCTCCAGAGGAGATATGTCAATCAGATGATCATCAATTAATGTCAAAAGCCCTGACTA 1663
QY 527 GAGAGGACCCCTCTAGAACATCAGAGATCATTAAGGAATTCCTTTGAATGTA 586
DB 1664 GAGAGGACCCCTCTAGAACATCAGAGATCATTAAGGAATTCCTTTGAATGTA 1723
QY 587 AGGACTGTGGGAAAGGCTTTAGTGTGGCTATCAACTTAAGTCAACATCAAGAAATCCATA 646
DB 1724 AGGACTGTGGGAAAGGCTTTAGTGTGGCTATCAACTTAAGTCAACATCAAGAAATCCATA 1783
QY 647 CTGGTGAGAAACCTTATGATGTAAAGATGTAAAGAGCCCTTCGTTGGGCAATCAGC 706
DB 1784 CTGGTGAGAAACCTTATGATGTAAAGATGTAAAGAGCCCTTCGTTGGGCAATCAGC 1843
QY 707 TTAATCAATCAAAAAATTCATATCTGGGAGAAAGCCCTACGAATGTAAAGACTGTGGGA 766
DB 1844 TTAATCAATCAAAAAATTCATATCTGGGAGAAAGCCCTACGAATGTAAAGACTGTGGGA 1901
QY 767 AGGCTTTTGGATGGGCTCAAGCCGTGTTATTCATTAAGAGATTCATCTAGTGAAGAAAC 826
DB 1902 AGGCTTTTGGATGGGCTCAAGCCGTGTTATTCATTAAGAGATTCATCTAGTGAAGAAAC 1961
QY 827 CCTATGAATGTAAAGACTGTGAAGAGCCCTTTCGGCGGTGTGATGAGCTCATCAGACCC 886
DB 1962 CCTATGAATGTAAAGAGTGTGGGAGGCAATGTAAACCATCTCCGAGAACATC 2021
QY 887 AGAGATTCCACATCTGGGAGAAAGACT 913
DB 2022 AGAGATTCCACACAGTTGAAGAGCCT 2048
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RESULT 6
US-09-881-578-3
Sequence 3, Application US/0981578
Publication No. US2003003966A1

GENERAL INFORMATION:
APPLICANT: Hering, Thomas
APPLICANT: Johnstone, Brian
TITLE OF INVENTION: PROBES FOR CHONDROGENESIS
FILE REFERENCE: 27708/04013
CURRENT APPLICATION NUMBER: US/09/881,578
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 2143
TYPE: DNA
ORGANISM: Homo sapiens
US-09-881-578-3

Query Match 34.9%; Score 703; DB 3; Length 2143;
Best Local Similarity 69.7%; Pred. No. 7.7e-206;
Matches 1006; Conservative 0; Mismatches 410; Indels 27; Gaps 3;

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QY 172 TTCACTTCTAATAACAATGCCCCAGGGTTTGTGACGTTCCGACGTAGCCATGACTTT 231
DB 10 TGCATTTCCAGAACCATGATGATGGTTTGTGACATTCAGGGATGTGGCCATGACTTC 69
QY 232 TCTCAGAGAGTGGGCTGTCTGAACTTCTCAGAGGAGCTGTACTGGAGCGTATG 291
DB 70 TCTCAGAGAGTGGGAGATGCTGACCTGTCTCAGAGGAGCTGTACTGGAGCGTATG 129
QY 292 CTGAGAACTACAGTAATCTGGTCTCACTGATTTGAGTCTC---AGCATATGAATAAAG 348
DB 130 TTGAGAACTATAGTACTGTTGTGCTCAGATTTTGAATGATCAAAACGATAGACCAA 189
QY 349 AGTTTACCTACAGAAAAAACATTCATGAATAAGGGCTTCCAAAGAAATTCAGATGA 408
DB 190 AAAATATTTTCAAGAAATGATATTTTGAATAAATTTTCCAGTGGAGATGAAGGAC 249
QY 409 AGAATTAATCCCTTGGCC-----GTACTGATATGTGAAGT 447
DB 250 AAAAGTAAACCCCTTGGCCCTGAGGATCATCTTCAGAAATATTTGAAGTGCAGAAAGC 309
QY 448 AGCTTGAAGAACCAAGGCTCCAGAGGAGTATGTCAATCAATGATCATCAATTAAT 507
DB 310 ATATTTGAGGAGCTTAAGAGACATCAAGAGGATCTTATAGTCAATGATTAATGACTAT 369
QY 508 GTCAAAAGGCTGTACTAGAGAGGACCCCTCTAGAACATCAGAGA---CATCAT 564
DB 370 GAAAAAATCCTTCTTACGAAAAAGTAAATCTTACTCCACATCAAGAAATTCATAAT 429
QY 565 AAGGAAATTCCTTGAATGTAAAGACTGTGGAAAGCCCTTTAGTGTGGCTATCAACTT 624
DB 430 ACGAGAAATCCTATGTTGTAAAGATGTGGAAAGGCTTGCAGTATGATGCTCAAAACTT 489
QY 625 AGTCACATCAAGAAATCATATCTGGTGAGAAACCTTATGAATGTAAAGATGTAAAG 684
DB 490 GTTCAACATGAGAGAACTATACGCTGAAGAAAGCACTTGAATGTAAAGATGTGGAAAG 549
QY 685 GCCTTCCTTGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTGGGAGAAAGCC 744
DB 550 AATTAATTAAGTGGCTATCACTCAATGTGATCAAGATTCATCTGGTGAAGAACCC 609
QY 745 TACGAATGTAAAGACTGTGGAAAGGCTTTTCATGTGGGCTCAAGCTCGTATTCATAAG 804
DB 610 TATGAGTGTAAAGATGTGGAAAGCCTTTAGCTGGGAGTCAAGCCTTGTATTAACATGAG 669
QY 805 AGGATTCATAGTGTGAAGAAACCTTATGAATGTAAAGACTGTGGAAAGGCTTGGCGGT 864
DB 670 AGAATTCACATGTGTGAAGAAACCTTATGAATGTAAAGATGTGGAAAGGCTTTAGTCT 729
QY 865 GGTATGAGCTCACTCAGACCAAGATTCACACTGGGAGAAAGACTACGAATGCATAA 924
DB 730 GGTATACACTTACCAACATCAGAAATTCATATTTGTGTGAATCTTATTAATGAAG 789
QY 925 GACTGTGGAGAGCCTTTAGCCGTGTATTAATCTTATTCAGACCAAGGAATTCATAGT 984
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Db 790 GATGTGGAGGCGCTTTTGGGGCTCAAGCCTTGCTAAACATGATTAATCATACA 849
Qy 985 GGGAGAGACCTTACGAGTGTAAAGACTGTGGAGGCTTTTATTTGGTTCAAGCTC 1044
Db 850 GGTGAGAACTTATTAATGTAAAGATGTGGAGGCTTCAAGTGTGATCAACTT 909
Qy 1045 ATTTCAGATAAAAGATTCAACAGGTGAAACCTTATGATATGCAAAAGTGGGAAG 1104
Db 910 ACTCAGCATCAGAAATCTACTGTATGAAACCTTATGAAATGTAAATATGTGAAAG 969
Qy 1105 GCCTTACTCGATCAATTACTTACTCAGCATCAGAAAGTCCACACCGGTGAGAGCT 1164
Db 970 GCTTTTGTGGGGCTATCACTTACTCGACATCAGATTTTCAATCTGTGAGAAACC 1029
Qy 1165 CACGAATGTAAGAGTGTGGGAAGGCTTTGCGTGGGTTCAAGCTCTTAAAGCAG 1224
Db 1030 TATGATGCAAGAAATGTGGGAAGGCTTTTAAATGCGATCAAGTCTTATTCACATGAA 1089
Qy 1225 AGGATACATACGGGGGAGAGGCGTTCAGTGCAGAGATGTGGAGGCTTCAATTGT 1284
Db 1090 ACAAATTCATACGTGTAGAAACCTTATGAAATGTAAAGATGTGAAAGGCTTTAGTGT 1149
Qy 1285 GGCATACCTCCTCAGACGAGAGATCCACACAGCGAAACCCCGTATTAATGTAG 1344
Db 1150 GGCATACCTTCTTCAACATCAGAAATCCATCTGTGTGAGAAACCTTTGAATGTAG 1209
Qy 1345 GAGTGTGGAGGCTTTCATTTATGTGATCAGCTTGTGAAACATGAGAAATTCATACC 1404
Db 1210 GAATGTGGAGGCTTTAGTTGGGGTTCAAGCCTTGTAAACATGAGAGTGTACTACT 1269
Qy 1405 GGGGTGAAACCTTATGGGTGTACAGAAATGTGGGAAGCTTTAGTACCGGCATCAGCTT 1464
Db 1270 GGTGAGAAATCCATGTAATGTAAAGATCGGAAAGACCTTTTGTAGTGGTATCAACTT 1329
Qy 1465 ACACAACATCAGAAACGACAGTGGGGGAGAACTTCAAGATGTAAAGATGTGGGAAG 1524
Db 1330 ACTCGACATCAGGTATTTCACTGTGTGAGAAACCTTATGAAATGTAGAAATGTGGGAAG 1389
Qy 1525 GCATGTACCACTTAACCATCTCCGAAACATCAGAGATCCACAAAGTTGAAGAGCC 1584
Db 1390 GCTTTAATTTGTGATCAAGCCTTGTTCAAATGAAAGATCCATCAGGGGAGAAACC 1449
Qy 1585 TTT 1587
Db 1450 TAT 1452

RESULT 7
US-10-623-914-3
/ Sequence 3, Application US/10623914
/ Publication No. US20050075495A1
/ GENERAL INFORMATION:
/ APPLICANT: Herings, Thomas M.
/ TITLE OF INVENTION: PROBES FOR CHONDROGENESIS
/ FILE REFERENCE: 27708/03905
/ CURRENT APPLICATION NUMBER: US/10/623, 914
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 2143
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-623-914-3

Query Match 34.9%; Score 703; DB 9; Length 2143;
Best Local Similarity 69.7%; Pred. No. 7.7e-206;
Matches 1006; Conservative 0; Mismatches 410; Indels 27; Gaps 3;

Qy 172 TTCAGTTCTTAAACAAATGGCCGAGGTTTGTGACGTTGCCGACGTCATAGCACTTT 231
Db 10 TCGAATTCAGAAACATGACTGATGGGTTGTGATTCAGGGAATGTGGCATCGACTTC 69

Qy 232 TCTCAGAGAGTGGGCTGTCTGAACCTCTCTCAGAGAGACCTGTACTGGAGCGTATG 291
Db 70 TCTCAGAGAGTGGGAATGCTGTGACCTGTCTCAGAGAGACTTGTACGTGATGTATG 129
Qy 292 CTGAGAACTACAGTAATCTGGTCTCACTGATTTGAGTCT---AGCATATGAAATTAAG 348
Db 130 TTGGAGAACTATAGTACTTGGTGTCACTGATTTGGATTCAAAACGTATGAGCCAAA 189
Qy 349 AGTTTACCTACAGAAAAAAACATTCATGAATTAAGGCTTCCAAAAGAAATTCAGATGA 408
Db 190 AAAATATTTTCAGAAAATGATATTTTGAATAATTTTCCAGTGGAGATGAAAGAC 249
Qy 409 AGAATTAATCCCTTGGCC-----GTAATGATATGTAAGT 447
Db 250 AAAAGTAAACCTTGGCTTGGAGCATCTTCAGAAATATGGAAGTCAAAAGC 309
Qy 448 ACGTTGAAAGACACACAGCGCTCCAGAGGAGTGTCAATCAGATGATCATCAATTAT 507
Db 310 ATATTGAGGAGCTTAAAGAGACATCAGAGGATCTTCAAGTCAATATATATCACTAT 369
Qy 508 GTCAAAAGGCTGTACTTAAAGAGGCAACCTCTCTAAGACATCAGAGA---CATCAT 564
Db 370 GAAAAATATCTTCTTACAGAAAAAGTAATCTTCTTACCATCAATCAAGAAATTCATAT 429
Qy 565 AAGGAAATTCCTTGAATGTAAAGACTGTGGAGAGGCTTTAGTGTGCTATCACTT 624
Db 430 ACAGAAATCCTATGTTGTAAAGAAATGTGGGAAGGCTTGACATCAGCTCAAAACTT 489
Qy 625 AGTCAACATCAGAAATCATCTGTGAGAAACCTTATGAAATGTAAAGATGTAAAG 684
Db 490 GTTCAACATGAGAACTATCAGCTGAAAGACCTTGAATGTAAAGATGTGGAG 549
Qy 685 GCCTTCGTTGGGGCAATCAGCTTCTCAACATCAAAATTCATATCTGGGAGAGCC 744
Db 550 AATTATTTAAGGCTTATCACTCAATGTGATCAGAGATTTTCAATCTGTGAGAAACC 609
Qy 745 TACGAATGTAAAGACTGTGGAGAGGCTTTGATGGGCTCAAGCTCGTTATTCATAG 804
Db 610 TATGATGTAAAGAAATGTGGGAAGCCTTTAGCTGGGATCAAGGCTTGTAAACATGAG 669
Qy 805 AGGATTCATCTGTGAAAAACCTTATGAAATGTAAAGCTGTGAAAGGCTTTGGGCT 864
Db 670 ABAATTCACACTGTGAGAAACCTTATGAAATGTAAAGATGTGGAGAGGCTTTAGTGT 729
Qy 865 GGTGATGAGCTCACTCAGACCAAGATTCACACTGGGAGAAAGACTACGATGCAAA 924
Db 730 GGCATCACTTACCAACATCAGAAATTCATATTTGGGTGAATCTTATTAATGTAG 789
Qy 925 GACTGTGGAGAGACTTTAGCCGTGTATTAACCTTATTCAGACAAAGAAATTCATAGT 984
Db 790 GAATGTGGAGGCTTTTGTGGGCTCAAGCCTTGTAAACATGAAATTAATTCATCA 849
Qy 985 GGGAGAGGCTTACAGAGTAAAGACTGTGGGAAGGCTTTATTTGTGTTCAAGCCTC 1044
Db 850 GGTGAGAACTTATTAATGTAAAGATGTGGAGGCTTCAAGTGTGCTATCAACTT 909
Qy 1045 ATTTCAGATAAAAGATTCAACAGGTGAAACCTTATGATATGCAAAAGTGGGAAG 1104
Db 910 ACTCAGCATCAGAAATCTACTGTATGAAACCTTATGAAATGTAAATATGTGAAAG 969
Qy 1105 GCCTTACTCGATCAATTACTTACTCAGCATCAGAAAGTCCACACCGGTGAGAGCTT 1164
Db 970 GCTTTTGTGGGGCTATCACTTACTCGACATCAGATTTTCAATCTGTGAGAAACC 1029
Qy 1165 CACGAATGTAAGAGTGTGGGAAGGCTTTGCGTGGGTTCAAGCTCTTAAAGCAGAG 1224
Db 1030 TATGATGCAAGAAATGTGGGAAGGCTTTTATTTGGATCAAGTCTTATTCACATGAA 1089
Qy 1225 AGGATACATACGGGGGAGAGGCGTTCAGTGCAGAGATGTGGAGGCTTCAATTGT 1284
Db 1090 ACAAATTCATACGTGTAGAAACCTTATGAAATGTAAAGATGTGAAAGGCTTTAGTGT 1149

QY 1285 GGCTATACCTCACTGAGACGAGAGATCCACAGCGGAAACCCGTAATTAATGTAAG 1344
 DB 1150 GGCTATACCTTCTTCAACATCAGAAATCCATACCTGTGAGAAACCTTTGTAATGTAAG 1209
 QY 1345 GAGTGGGAAAGGCTTCACTTATGATGAGGCTGTGAAACATAGAGAAATTCATACC 1404
 DB 1210 GATGAGGAAAGGCTTGTAGTGGGATCAAGCCTTTGTAACATAGAGAGATTCATACC 1269
 QY 1405 GGGGTAAACCCATGAGTGTATCAGAAATGAGAAAGCTTTAGTACCGGCTACAGCTT 1464
 DB 1270 GGTGAGAAATCCATGATGTAATGAAATGGGAAAGACCTTTGTAGTGGATTCATCTT 1329
 QY 1465 ACACAACATCAGAAACGACAGTGGGCGAAATCCTACGATGTAAAGAGTGGGAAAG 1524
 DB 1330 ACTGCATCAGGATTTTCACTGCTGTGAGAAACCTATGATGTAAAGAAATGGGAAAG 1389
 QY 1525 GCATGTAAACCTTAACCATCTCCGAGAACATCAGAGATTCACAAACGTTGAAGACC 1584
 DB 1390 GCTTTTAATTTGGATCAAGCCTTTGTTCAACATGAAAGAAATCCATCAAGGGAGAAACCC 1449
 QY 1585 TTT 1587
 DB 1450 TAT 1452

RESULT 8

US-10-094-749-1120

Sequence 1120, Application US/10094749

Publication No. US20030219741A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKI, ICHIRO
 APPLICANT: SEKI, NAOHICO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTOKUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
 FILE REFERENCE: 084335/0160
 CURRENT APPLICATION NUMBER: US/10/094,749
 PRIOR FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: 60/350,435
 PRIOR FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: JP 2001-328381
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 3381
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1120
 LENGTH: 1945
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-094-749-1120

Query Match 30.7%; Score 618; DB 6; Length 1945;

Best Local Similarity 65.8%; Pred. No. 1,56-179;

Matches 956; Conservative 0; Mismatches 470; Indels 26; Gaps 3;

QY 145 GGAACCCCGAGAGACTGATCAGTTCTT--CAGTTTAAACAAATGAGCCAGGGTTGG 202
 DB 217 GGAACCCAGAGAGACTGATCAGTTCTTCTGCAAGCTTAAACAAATGAGCCAGGGTTAG 276
 QY 203 TGAAGTTGCCGAGAGTACCATATGATCTTTTCTCAGAGAGAGTGGCTGTGTAATCTTG 262

DB 277 TGAATGTCAGGAGATGTGTCATTTGACTTCTCAGAGAAAGTGGAAATGCTGAGCTTG 336
 QY 263 CTCAGAGGAGCTGTACTGAGAGCTGATGCTGAGAAATCTACATGATCTTGCTCACTGG 322
 DB 337 CTCAGAGAGATTTGATAGAGATGTGATGCTGAGAAATCTATGCAACTTGTATCACTAG 396
 QY 332 ATTGAGTCAAGCATATGAAATTAAGATTATCTACAGAAAAAAACATTCATGAATTA 382
 DB 397 ACTTGCTTCAAGAGTGTGCAATTAAGACTTATCTCCAGAAAAAAGCACTTATGAAGACAG 456
 QY 383 GGGCTTCCAAAAGAAATTCAGATAGAAAGTAAATCCCTTG----- 424
 DB 457 AATTATCCCAATGGGAAATAGATGACAGCTTGAATACTGATCTTGAGAGTCCATT 516
 QY 425 ---GCCGTAATGATATGAGAGTACGCTTGAAGACACAGAGCTCCAGAGGAGGT 481
 DB 517 CAGAGGATTTTGTGAAGCCAAAGCCAGATGAGAGAGCAAGAAATCAGAAAGAT 576
 QY 482 ATGTCAATCAGATGATCATCAATTATGCAAAAGGCTGCTACTAGAGAGGACCCCTC 541
 DB 577 ATTTGAGCAGAGGATGATCATATATGACAAATGTCATTTCACACGATCTACTACT 636
 QY 542 CTAGAAACATCAGAG---CATCATAGAGAAATTCCTTGAATGTAAGGACTGAGGA 598
 DB 637 TATCTCAACATTCAGAGTCAATTTCTACGAGAAACCTATTAATGTAAATGAGATGGGA 696
 QY 599 AGGCTTTAGTGTGCTATCACTTACATCAATCAGAAAAATCCATCTGTGTGAGAAAC 658
 DB 697 AAGCTTCAGAGAGCTCAGACCTAACCAACATCAATGATTTATATCTGTGAGAAAAAC 756
 QY 659 CTTATGATGTAAAGATGTAAAGAGCCTTCGTTGGGCAATCAGCTTACTCAATC 718
 DB 757 CTTATGATGTAAAGCAATCGGGAAGCCTTTAGTGTATTCACAACTCAGCTTCAATC 816
 QY 719 AAAAAATTCATCTGGGGAAGACCCCTAGAAATGTAAAGCTGTGGAGGCTTTGCAT 778
 DB 817 AGAGACTTATCTGCTGAGAAACCTATGCAATGTAAAGATGTGGAAAGCCTTTATCTC 876
 QY 779 GGGGCTCAAGCTCGTTATTTCAAGAGATTCATCTGCTGTAAGAAAACTTATGAATGTA 838
 DB 877 AAGCTCAACATTTATTTACATCAATGAAATTCATCTGTGAAAAACCATTAATATGTG 936
 QY 839 AAGACTGTGAAAGGCTTTCCGCTGTGTATGAGCTCACTGACCAAGATTCACA 898
 DB 937 AAGATGTGGAAAGGCTTTATTCGTAAGCTCAACATTCACGACATCAAAAAGTTCATA 996
 QY 899 CTGGGAGAAAGCTACGATGCAAGAGCTGTGGGAAGCCTTTAGCCGTGTATTAAC 958
 DB 997 CTGTGAGAAAGCTTATGAAATGTAAAGATGTGGAAAGCCTTTACTCAGAAATTCACAC 1056
 QY 959 TTATTCAGCAAGAGAAATTCATAGTGGGAGAGCCTTACGATGTAAAGACTGTGGGA 1018
 DB 1057 TTAACATACACAGAGACTTCACTGCTGGAAGAGCTCATGATGTAAAGATGTAGGA 1116
 QY 1019 AGGCTTTTATTTGTGTTCAAGCTTATTCAGATTAAGAAATTCACAGAGTGAAGAAC 1078
 DB 1117 AGGCTTTTACTAGCTCTCAACATTAATCTGCAATGAAGAAATTCATACCGGTGAAGAAC 1176
 QY 1079 CCTATGAATGTCAAGAAATGTGGGAAGCCTTTACTGATGATCAATTCCTTACTCAGATC 1138
 DB 1177 CCTATGAATGTGAAGAAATGTGGAAAGCCTTTATTTGTGCTCAGAGCTTCTCAACATC 1236
 QY 1139 AGAAGATCCACACCGGTGAGAAAGCTCAGAAATGTAAAGATGTGGAAAGGCTTTGCT 1198
 DB 1237 AGAAATTTCAATATGGGAAAAACCATATGATGTAAAGAAATGTGAAGGCTTTATTC 1296
 QY 1199 GGGGTTCAAGCTCGTTAAGCAGAGAGATCATACGAGGAGAAAGCCGTACAGTGA 1258
 DB 1297 GGGGCTCACTAGATGACAAATCAGAGATTCATCTGTGTGAAGAAACCTTATTAATATGTG 1356
 QY 1259 CAGAAATGTGGAAGGCTTCAATTTGTGCTATCACTCACTCAGCAAGAGAAATCCACA 1318

Db 1357 AAGATGTGGGAAGGCTTTATCCGTGGCTCAAACTTACGACACGAGAAATTCACA 1416
Qy 1319 CAGCGGAAACCCGTAATAATGTAAAGAGTGTGGGAAGGCTTCAATTATGATGAGCC 1378
Db 1417 CCAATGAAAGCCCTATGATGTAAAGATGTGGAAAGATGTTAGTCATGCTCAAC 1476
Qy 1379 TCGTAAACATGAGGAATTCATACCGGGGTGAAACCCATGAGGTGACAGAAATGTGGGA 1438
Db 1477 TTACTCAACATGAGGAATTCACACTGGTGAAGAAACCTTATCAATGTAAAGAAATGTGGA 1536
Qy 1439 AGAGCTTATGTCACGGCCATCACTTACCAACATCAGAAACGACAGTGGGGGAAAT 1498
Db 1537 AAGCTTTATATGTGGCTCACTCTTACACGACACAGAGATTCATCTGGTGAAGAAC 1596
Qy 1499 CCTACGAATGTAGAGTGTGGGAAAGGATGTAAACCACTTAACCATCTCCGAGAACATC 1558
Db 1597 CCTAGGAATGTAAAGAAATGTGAAAAACCTTTATGCTGTGCTCAGAACTTACTCAACATG 1656
Qy 1559 AGAGATCCACA 1570
Db 1657 AGCGAATTCACA 1668

RESULT 9

US-10-108-260A-2359
; Sequence 2359, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2359
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2359

Query Match 30.5%; Score 615.4; DB 6; Length 2235;
Best Local Similarity 75.3%; Pred. No. 1e-178;
Matches 766; Conservative 0; Mismatches 251; Indels 0; Gaps 0;

Qy 559 CATCATTAAGGAGAATTCCTTGAATGTAAAGACTGTGGGAAGCCTTTAGTGTGGCTAT 618
Db 894 CATACTGTGTGAGAAACCTATGATGTAAAGATGTGGGAAGCCTTTAGTGTGGGATCA 953
Qy 619 CAACCTTATGTCACATCAGAAATCCATATCTGTGTGAGAAACCTTATGATGTAAAGATGT 678
Db 954 AGCCTTGTAAACATGAGGAATTCACACTGTGTGAGAAACCTTATGATGTAAAGATGT 1013
Qy 679 AAGAGAGCCTTCGTTGGGGCAATCAGCTTACTCAACATCAAAAATTCATCTGGGGAG 738
Db 1014 GGGAAAGCCTTTATGCTGTGTGATCACTTACCAACATCAAAAATTCATCTGGGTG 1073
Qy 739 AAGCCTTATGATGTAAAGACTGTGGGAAGCCTTTTCATGTGGGCTCAAGCCTCGTTAT 798
Db 1074 AATCTTATTAATGTAAAGATGTGGGAAGCCTTTTGTGGGGCTCAAGCCTTGTCTAA 1133
Qy 799 CATTAAGAGATTCATCTGTGTGAAAAACCTTATGATGTAAAGACTGTGAAAAAGCCTTT 858
Db 1134 CATGAGATTAATTCATCAAGGTAGAAACCTTATTAATGTAAAGATGTGGGAAGCCTTTC 1193
Qy 859 CGCGCTGTGTAGAGTCACTCAGACACAGATTCACACTGTGGGAGAAAGACTATCAGAA 918
Db 1194 ATCTGTGGCTATCACTTATCTCAGATCAGAAATTCATCTGTGTAAAGAAACCTTATGAA 1253
Qy 919 TGCAGAGACTGTGGGAAGCCTTTAGCGTGTGTATAACTTATTCAGACAAGAGATTT 978
Db 1254 TGTAAATATGTGGAAGCCTTTTGTGTGGGCTATCACTTATCTGACATCAGATATATT 1313

Qy 979 CATATGTGGGAGAAAGCCTTTACAGATGTAAAGACTGTGGGAAGGCTTTTATTGTGTCTCA 1038
Db 1314 CATACTGTGTGAGAAACCTTATGATGTCAAGAAATGTGGGAAGCCTTTTATTGTGGGATCA 1373
Qy 1039 AGCCTCATTTACAGATTAAGAAATTCACACAGGTGAGAAACCTTATGAAATGTCAAGATGT 1098
Db 1374 AGCTTATTAACAACATGAAGAAATTCATCTGTGTGAAACCTTATGATGTAAAGATGT 1433
Qy 1099 GGGAAAGCCTTTATCTCGAGTCAATTACTTACTCAGATCAGAAATTCACACCGGTGAG 1158
Db 1434 GGAAGAGCCTTTATGCTGTGTATCACTTCTCAACATCAGAAATTCATCTGTGTAG 1493
Qy 1159 AAGCTTCAGATGTAAAGAGTGTGGAAGGCTTTCGTGGGCTTCAGAGCCTCGTTAAG 1218
Db 1494 AATCTTTGATGTAAAGAAATGTGGGAAGCCTTTATGTTGGGCTTCAAGCCTTGTAA 1553
Qy 1219 CACGAGAGATATCATACGGCGAGAAAGCCTTCAAGTCAACAAATGTGGGAAGCCTTTC 1278
Db 1554 CATGAGAGATTCATATCTGTGTGAGAAATCCATGAAATGTAAAGATGTGGGAAGCCTTT 1613
Qy 1279 AATTGTGCTATCACTCAGTCAAGAGATTCACACAGGCGAAACCCGTAATAA 1338
Db 1614 TGTAGTGGGTATCACTTATCTGACATCAGATGTATTCACACTGTGTGAGAAACCTTATGAA 1673
Qy 1339 TGTAAAGAGTGTGGGAAGCCTTTCATTTATGATGAGCTCGTGAACATGAGAGAAAT 1398
Db 1674 TGTAAAGAAATGTGGGAAGCCTTTTATTTGTGATTAAGCCTTGTTCACATTAAGAAATC 1733
Qy 1399 CATACCGGGGTGAAACCTTATGGTGTGACAGAAATGTGGGAAGCCTTTATGACCGGCT 1458
Db 1734 CATACAGGGGAGAAACCTTATGAATGTAAAGATGTGGGAAGCCTTTATGCTGTGGCTAT 1793
Qy 1459 CAGCTTATCAACATCAGAAACGACAGTGGGCGAAATCTTACGAATGTAAAGATGTGC 1518
Db 1794 CACCTTATCAACATCAGAAATTCATACCGGTGTGAAACCTTTCAAAATGTAAAGAAATGT 1853
Qy 1519 GGGAGAGATGTAAACCATCTCGAGAACATCAGAGATCCACAACAGT 1575
Db 1854 GGGAAAGCCTTTCAGTGGGGTTCAGAGCTTATGATGACATGAGAGTCCATATCTAAT 1910

RESULT 10

US-10-450-763-25299
; Sequence 25299, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 25299
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (28)..(1464)
; OTHER INFORMATION: 60% homologous to Homo sapiens zinc finger protein, accession
; OTHER INFORMATION: number X78933, Smith-Waterman Score=1602.
US-10-450-763-25299

Query Match 30.0%; Score 603.6; DB 9; Length 1900;
Best Local Similarity 70.3%; Pred. No. 4.2e-175;
Matches 823; Conservative 0; Mismatches 344; Indels 3; Gaps 1;

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QY 429 TAACTGATATGTGAAGTACGCTTGAAAAGACACAGCGCTCCAGAGGAGATATGTCAA 488
DB 51 TAAATGGAGGTGAAGAGCAATATCGAGGACATAAAGGACATCAAGAGGAACTCTCAG 110
QY 489 TCAGATGATCATCAATTAATGTCAAAAAGCGCTGTACTAGAAAGCAACCCCTCTTGAAC 548
DB 111 TCAAAATGATATCAGCTATGAAAAAATACCTTCTCAGAAAAAGTAAATCTTCTCTCC 170
QY 549 ACATCAGACA---CATCATAGGAGAAATCCTTGAATGTAAAGACCTGTGGGAAGGCTT 605
DB 171 ACATCAAGAAATTCATTAATACAGAAATCTAATGTTTGAAGAAATGTGGGAAGGCTTG 230
QY 606 TAGCTGTGCTATCAACTAGTCAACATCAGAAAATCACTACTGTGTAGAAACCTTATGA 665
DB 231 CAGTCAATGCTCAAACTTGTTCACATAGAGAACTCAATACAGCTGAAAAAACCTTTGA 290
QY 666 ATGTAAAGATGTGAAGAGCGCTTCGGTGGGCAATCAGCTTACTCAATCAATCAAAAAT 725
DB 291 ATGTAAAGATGTGGGAAGAAATTAATTAAGTGCCTATCAACTCAATGTGCATCAGAGAT 350
QY 726 TCATCTGGGGAGAACCCCTAGCATGTAAAGACTGTGGGAAGGCTTTCGATGGGGCTC 785
DB 351 TCATCTGGTGAAGAACCCCTATGATGTAAAGATGTGGGAAGACCTTTAGCTGGGAGTC 410
QY 786 AAGCTCTGTATTCATTAAGAGATTCATCTGTGAAAAACCTTATGAATGTAAAGACTG 845
DB 411 AAGCTTGTTAACATGAGAGATTCACCTGTGAGAAACCTTATGAATGTAAAGATG 470
QY 846 TGGAAAGCGCTTTCGGCGTGTGTATGAGTCACTCAGCACAGAGATTCACACTGGGA 905
DB 471 TGGGAAGCGCTTATGTCGTGCTATCACTTACCACATCAAAAAATTCATCTGTGT 530
QY 906 GAAAGCTACGATGTGAAGACTGTGGGAAGACCTTTAGCGGTGATTAATCTTATCA 965
DB 531 GAAATCTTAAATGTGAAGAAATGTGGGAAGCGCTTTTGGGGCTCAAGCGCTTGCTAA 590
QY 966 GCACAAGAGATTCATAGTGGGGAAGACCTTACGAGTGTAAAGACTGTGGGAAGCTTT 1025
DB 591 ACATGAGATTAATTCATACAGTGAAGAACTTAAATGTAAAGATGTGGGAAGCGCTT 650
QY 1026 TATTTGTGTTCAAGCCTCATTCAGCTAAAGAAATTCACACAGTGTGAAGAACCTTATGA 1085
DB 651 CAGTCTGTGCTATCAGCTTACTCAGCATCAAAAAATTCATATGTGAAGAACCTTATGA 710
QY 1086 ATGTCAAGATGTGGGAAGCGCTTACTCGAGTCAATTAACCTTACTCAGATCAGAGAT 1145
DB 711 ATGTAAATATATGTGAAGAGCGCTTTTGTGGGCTATCACTTCTGACATCAATATTT 770
QY 1146 CCAACCGGTGAGAAAGCGCTCAGAAATGTAAAGAGTGTGGGAAGCGCTTTCGCTGGGTTT 1205
DB 771 TCATATCGTGTGAAGAACCTTATGATGCAAGAAATGTGGGAAGCGCTTTTAAATGGGATC 830
QY 1206 GAGCTCTGTAAAGCAGAGAGATCATACGGCGGAGAAAGCGCTTCAAGTGCACAGATG 1265
DB 831 AAGCTTATTCACATGAAAGAAATTCATCTGTGTGAAGAAACCTTATCAATGTAAAGATG 890
QY 1266 TGGGAAGCGCTTCAATGTGGCTATCACTCAGCTCAGACAGAGAGATTCACAGGCGA 1325
DB 891 TGAAGAGCGCTTATATGTGTGTATCACTTTCTCAACATCAGAAAAATTCATCTGTGTA 950
QY 1326 AACCCGCTATAAATGTAAAGAGTGTGGGAAGCGCTTTCATTTATGATCGAGCGCTGAA 1385
DB 951 GAAACCTTTTGAATGTAAAGAAATGTGGGAAGCGCTTTAGTTGGGCTTCAAGCGCTGTTAA 1410
QY 1386 ACATGAGAGATTCATACCGGGGTGAACCTTATGSGGTATCAGATGTGTGAAGAGCTT 1445
DB 1011 ACATGAGAGATTCATCTGTGTGAAGATCCATGAAATGTAAAGAAATCGGGAAGACCTT 1470
QY 1446 TAGTCAACGGGCATCAGCTTACAAACATCAGAAAAGCAGACAGTGGGGCGAAATCTTACGA 1505
DB 1071 TTGTAGTGGGTATCACTTACTCGACATCAGGATTTTTCACACTGTGTGAAGAACCTTATGA 1130
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QY 1506 ATGTAAAGAGTGGGGAAGGATGTAAACCACTTAAACCATCTCCGAGAAATCATCAGAGAT 1565
DB 1131 ATGTAAAGAAATGTGGGAAGCGCTTTAAATGTGTGATCAAGACCTTGTTCACATGAAGAAT 1190
QY 1566 CCACAACAGTTGAAGAGCGCTTTTGAACGCA 1595
DB 1191 CCATACAGGGGAGAAACCTTATGAAGATGA 1220

RESULT 11
US-09-764-864-567
; Sequence 367, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PRZ23
; CURRENT APPLICATION NUMBER: US/09/764, 864
; PRIOR APPLICATION DATA: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 567
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (745)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-567

Query Match 29.5%; Score 593.6; DB 3; Length 774;
Best Local Similarity 91.4%; Pred. No. 3.1e-172;
Matches 690; Conservative 5; Mismatches 25; Indels 35; Gaps 5;

QY 1 CGCTTGTGACCGGTGACGCAACCGCTGTGTCTCCGCGCATGCCGAGGCCAGCATCTCT 60
DB 18 CGCTTGTGACCGGTGACGCAACCGCTGTGTCTCCGCGCATGCCGAGGCCAGCATCTCT 77
QY 61 TCAGAAAGACATCCCGGAGGAGAAAGCATTCGTTAAACATCTTAAGTC----- 111
DB 78 TCAGAAAGACATCCCGGAGGAGAAAGCATTCGTTAAACATCTTAAGTCAGCTTTACC 137
QY 112 -----AGCTTACGCTCTCGGAATTTGTCTTCTTCACTGTGAAG 150
DB 138 AGTGAAGAAACGACACTGTGAGCTTACGCTCTCGGAATTTGTCTTCTTCACTGTGAAG 197
QY 151 CCCGAGAAAGCTGATCAATTTCTTCACTTCTTAAACATGCGCCAGGCTTTGTGACGTTT 210
DB 198 CCCGAGAAAGCTGATCAATTTCTTCACTTCTTAAACATGCGCCAGGCTTTGTGACGTTT 257
QY 211 GCCGAGTGAAGCACTGATCTTTCTCAGGAGAGTGGGCGGTGTGAACCTGTCTCAGAGG 270
DB 258 GCCGAGTGAAGCACTGATCTTTCTCAGGAGAGTGGGCGGTGTGAACCTGTCTCAGAGG 317
QY 271 GACCTTACTGGGACCTGTATGCTGTGAAGACTACATGATCTTGTCTCACTGTGATTTGAG 330
DB 318 GACCTTACTGGGACCTGTATGCTGTGAAGACTACATGATCTTGTCTCACTGTGATTTGAG 377
QY 331 TCAGCATATGAAAAATTAAGAGTTTACTTCAAGAAAAAAACATTCATGATAAATAGGCTTCC 390
DB 378 TCAGCATATGAAAAATTAAGAGTTTACTTCAAGAAAAAAACATTCATGATAAATAGGCTTCC 437
QY 391 AAAAGGAATTCAGATGAAGAGTAATCCCTTGGCGGTAACTGTGAATGTGAAGGTAAG 450
DB 438 AAAAGGAATTCAGATGAAGAGTAATCCCTTGGCGGTAACTGTGAATGTGAAGGTAAG 497
QY 451 CTTGAAGAACCAAGAGCTTCAAGAGGAGTATGTCAATCAGATGATCAATTAATGTTC 510
DB 498 CTTGAAGAACCAAGAGCTTCAAGAGGAGTATGTCAATCAGATGATCAATTAATGTTC 557
QY 511 AAAAGCGCTGTCTATGAGAAAGGCAACCTCTTGAACAATCAGAGACATCATTAAGAG 570
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Db 558 ATAGGCTGCTGCTAGTGAAGAGCACCCTCTTAAGACATCAAGACATCATTAAGSG 617
Qy 571 AATTCCTTTGAATGTAGAGACTGTGGAAAGCCCTTTAGTCGT-GGCTATCAACTTAA-TC 628
Db 618 AATTCCTTTGAATGTAGAGACTGTGGAAAGCCCTTTAGTCGTGGGTATCAACTTAAGTTC 677
Qy 629 AACATCAAGAAATCCATCTGCT-GAGAAACCTTTATGATGT--AAAGATGTAAAGAG 685
Db 678 AACATCAAGAAATCCATCTGCTGAGAAACCTTTATGATGTAAAGATTTTAAAGAGAG 737
Qy 686 CCTTCGTTGGGGCAATCAGCTTACTCAACATCAA 720
Db 738 GCCTTCNTTTGGGGCAATCCAGCTTTACTTCAA 772

RESULT 12
US-10-029-386-13162
; Sequence 13162, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13162
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: g14758021, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q14585, EVALUE 1.00e-48
; OTHER INFORMATION: EST_HUMAN HIT: BE742835.1, EVALUE 0.00e+00
US-10-029-386-13162

Query Match 29.0%; Score 584.4; DB 6; Length 592;
Best Local Similarity 99.8%; Pred. No. 1.8e-169;
Matches 585; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GATTGGAGTCGATATGAAATAAGATTCTTACCTACAGAAAAACATTCATGAATA 381
Db 7 GATTGGAGTCGATATGAAATAAGATTCTTACCTACAGAAAAACATTCATGAATA 66
Qy 382 AGGGCTTCCAAAAGAAATTCAGATGAAGAACTAATCCCTGGCCGTAACCTGATATGT 441
Db 67 AGGGCTTCCAAAAGAAATTCAGATGAAGAACTAATCCCTGGCCGTAACCTGATATGT 126
Qy 442 GAAGGTACGCTTGAAGACACAGAGCTCCAGAGGAGGTATGTCATTCAGATGATCATC 501
Db 127 GAAGGTACGCTTGAAGACACAGAGCTCCAGAGGAGGTATGTCATTCAGATGATCATC 186
Qy 502 AATTATGTCAAAAAGCCTGCTACTAGAGAGGACCCCTCTTGAACAACATCAGAGACAT 561
Db 187 AATTATGTCAAAAAGCCTGCTACTAGAGAGGACCCCTCTTGAACAACATCAGAGACAT 246
Qy 562 CATAAGAGAAATTCCTTTGAATGTAGAGACTGTGGGAAAGCCCTTATAGTCGTGCTATCAA 621
Db 247 CATAAGAGAAATTCCTTTGAATGTAGAGACTGTGGGAAAGCCCTTATAGTCGTGCTATCAA 306
Qy 622 CTTAGTCAACATCAGAAAAATTCATCTGTGTGAAACCTTATGAATGTAAAGATGTAG 681
Db 307 CTTAGTCAACATCAGAAAAATTCATCTGTGTGAAACCTTATGAATGTAAAGATGTAG 366

Qy 682 AAGGCTTCGGTTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTAGTGGGAGAAG 741
Db 367 AAGGCTTCGGTTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTAGTGGGAGAAG 426
Qy 742 CCTACGAATGTAAAGACTGTGGGAAAGCCCTTTGATGAGGAGCTCAAGCCCTGTAATTCAT 801
Db 427 CCTACGAATGTAAAGACTGTGGGAAAGCCCTTTGATGAGGAGCTCAAGCCCTGTAATTCAT 486
Qy 802 AAGAGATTCATCTGTGTGAAAAACCTTATGAATGTAAAGCTGTGGAAGAGCCCTTTGG 861
Db 487 AAGAGATTCATCTGTGTGAAAAACCTTATGAATGTAAAGCTGTGGAAGAGCCCTTTGG 546
Qy 862 CGTGTGATGAGCTCAGCTCAGACCAAGATTCACATCTGGGGAGA 907
Db 547 CGTGTGATGAGCTCAGCTCAGACCAAGATTCACATCTGGGGAGA 592

RESULT 13
US-10-786-148-116
; Sequence 116, Application US/10786148
; Publication No. US20050191634A1
; GENERAL INFORMATION:
; APPLICANT: LIN, SHIU-RU
; APPLICANT: MANG, JAM-YUAN
; TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER
; FILE REFERENCE: BHT/3230-85
; CURRENT APPLICATION NUMBER: US/10/786,148
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 116
; LENGTH: 3163
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-148-116

Query Match 27.1%; Score 546; DB 9; Length 3163;
Best Local Similarity 69.3%; Pred. No. 3.9e-157;
Matches 772; Conservative 0; Mismatches 340; Indels 2; Gaps 2;

Qy 487 AATCAGATCATCATTAATTAATGTCAAAAGGCTGTCTTACAGAGAGGACCCCTCTTGA 546
Db 642 AATCAGATCATCATTAATTAATGTCAAAAGGCTGTCTTACAGAGAGGACCCCTTAC 700
Qy 547 AACATCAAGACATCATTAAGAGAAATTCCTTGAATGTAAAGACTGTGGAAAGCCCTTT 606
Db 701 CATCAAGAAATTCATCTAGTGTAGAGAGCCCTTTGATGTAAAGATGTGGAAAGCCCTTT 760
Qy 607 AGTGTGCTATCAACTTATGTCACATCAGAAAAATCCATCTGTGTGAGAAACCTTATGAA 666
Db 761 AGTGTGCTATCAACTTATGTCACATCAGAAAAATCCATCTGTGTGAGAAACCTTATGAG 820
Qy 761 TGTAAAGAAATGTAAAGAGCCCTTCGTTGGGGCAATCAGCTTACTCAACATCAAAAAAT 726
Db 821 TGTAAAGAAATGTAAAGAGCCCTTTATGTTTGTGATCAGCCCTTATTCACATCAATCAT 880
Qy 821 CATACTGGGAGAAAGCCCTTACAGAAATGTAAAGACTGTGGAAAGCCCTTTGATGGGCTCA 786
Db 881 CACAGTGTGAGAGCCCTTATGATGTAAAGATGTGGAAAGTCCCTTATGTTGAATCA 940
Qy 787 AGCTTCGTTATTCATTAAGAGATTCATCTGTGAAAAACCTTATGATGTAAAGACTGT 846
Db 941 GACCTTATTCGCAATCAGAAATTCACAGAGTGAAGAACTTATGAAATGTAAATTTGT 1000
Qy 847 GGAAGAGCCCTTTGGCGTGTGATGAGCTCACTGACACCAAGATTCACACTGGGAG 906
Db 1001 GGTAAAGCCCTTTGGCGAGTGTTCAAACCTTATCAACATCCGCGGATTCATCTAGTGTAG 1060
Qy 907 AAAGACTACGAATGTCAAGAGCTGTGGGAAAGCCCTTATGAGCTGTGTATTAATTTAG 966
Db 1061 AAACCTTATGATGTCAAGAGCATGTGGATGAGCCCTTATGACAGTGTGTCCGCTTATCCGG 1120
Qy 967 CACAAGAAATTCATAGTGTGGGAGAGCCCTTACAGAGTGTAAAGACTGTGGGAAAGCCCTTT 1026

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Db      1121 CATCAGAGATTCATACCGGTGAGAAACCATATATATGTAAGATGTGTAAGGCTTT 1180
Qy      1027 ATTGTGTTCAAGCTCATTTGAGCTAAAGAAATTCACACAGGTGAGAAACCTATGAA 1086
Db      1181 AGTTTGGATCGACCTTTACTGACATCAAAAGATTCATCTGGTGAAGAACCTTATGTA 1240
Qy      1087 TGTCAAGATGTGGAGAGGCTTTTACTCGAGTCAATTAACCTTACTGAGCATGAGAGATC 1146
Db      1241 TGTAAAGATGTGGAGAGGCTTTTATATGTCAGATCTCACTCAGATCAGAGAAAT 1300
Qy      1147 CACACCGTGAGAGGCTTCACGATGTAAGAGGTGGAGAGGCTTTGCTGGGGTTG 1206
Db      1301 CACACTGGTGAGAAACCTATGAGTGTAAAGAGTGAAGAACCTTTAGAAAGTGTTCA 1360
Qy      1207 ACCCTGTTAAGCAGAGAGATCATAGGGGAGAAACCTTACAAAGTGCACAGATGT 1266
Db      1361 AACTTATTCACATCAAAAGATGCACTGAGAGAAACCTTATGATGTAAGATGT 1420
Qy      1267 GGAAGAGCTTCATTTGTGGCTATCACTCACTCAGACAGAGAAATCCACAGGCGAA 1326
Db      1421 GGAAGACCTTTATAGTGTGTTCAAGCTTACTCAACATCAAGAAATTCATCTGGTGA 1480
Qy      1327 ACCCGTATTAATGTAAGAGTGTGGAGAGGCTTTCAATTATGATCGAGCTCGTAA 1386
Db      1481 AAACCTATGAATGTAAAGATGTGGAGAGGCTTTGTAGTGGCTCAAAACCTTATCAA 1540
Qy      1387 CATGAGAAATTCATCCGGGGGTGAACCTTATGGGTGTAACGAAATGTGGAGAGCTTT 1446
Db      1541 CACCACTATATCATATGTTGGTGAAGACCTTATGAATGTAAGAAATGTGAAAGTCTTT 1600
Qy      1447 AGTCAGGCGCATCAGCTTACACAACATCAGAAACGACAGTGGGGCGAAATCTTACGA 1506
Db      1601 AGTAGGTGTTCAAGCTTTTATGCGCACAGAGATTCACACTGGTGAAGAACCTTATGA 1660
Qy      1507 TGTAAAGAGTGGGGAGGCAATTAACACTTAACCATTCGAGAAATCAGAGAGATC 1566
Db      1661 TGTAAAGAGTGTGGAGAGGCTTTTATGAGCTCAAGCCTTACTGACATCAGAGAAAT 1720
Qy      1567 CACACAGTGAAGAGCCTTTGAAGCAGTAC 1600
Db      1721 CA-TACAGGTGAGAAACCTTATGATGTAAGAAC 1753

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RESULT 14

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US-10-221-625-162
; Sequence 162, Application US/10221625
; Publication No. US2004003942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dying, Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: WATKINS, Preeti
; APPLICANT: SHAH, Purvi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PP-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221,625
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 162
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US2004003942A1 2154810CB1
US-10-221-625-162

Query Match      26.7%; Score 538.6; DB 7; Length 1813;
Best Local Similarity 69.0%; Pred. No. 5.4e-155;
Matches 793; Conservative 0; Mismatches 329; Indels 27; Gaps 3;

Qy      322 GATTGAGTGCATATGAAATTAAGATTACTTACAGAAAGAAACATTCATGAATA 381
Db      377 GATTGAGAGCCAGATGATGAGCCAGAAAGTTATCTTAAAGAAATGACATTTATGAATA 436
Qy      382 AGGCGTTCCAAAAGAAATTCAGATGAAGAAAGTAAATCCCTTGGCCGTAAAC----- 432
Db      437 AATTATCCAGTGAAGTAAATGAAAGAAATTTGAAACCATAGCCTTAAGGCTCAT 496
Qy      433 -----TGAATATGTAAGATACGCTTGAAGAACCCAGCGCTCCAGAGAGAG 480
Db      497 TTAAGAAATGATTTGGAAATCCACAGAAAGAAATTTGAAGACAGAGAGACCTCAAGAGGA 556
Qy      481 TATGTCATCAGATGATCATCAATTATGTCAAAAGGCTGCTACTAGAGAGGACCCCT 540
Db      557 TACTTCAATGATGTAAGAAATGCAATCTGAAAGTGTCTCTTACAGAAAGGACATCT 616
Qy      541 CCTAGAACATCAGAGACATCA---TAAGAGAAATTCCTTGAATGTAAGACTGTGG 597
Db      617 GTTATCCCATCAGAGACCTTATTTGTGTAAGAAACCTTATGAATGTAAGAAATGTGG 676
Qy      598 AAGCGCTTTAGTGTGCTGCTATCACTTACTCAATCAAGAAATCCATCTGTGAGAA 657
Db      677 AAGCGCTTACAGTGTGCGCCACAGCTTACTTTCATCAAGAAATCATCTGTGAGAA 736
Qy      658 CCTTATGAATGTAAGAAATGTAAGAGGCTTCCTGTGGGCAATCAAGCTTACTCAACAT 717
Db      737 CCGTATGAATGTAAGAAATGTAAGAGGCTTTCAGAGACATCTGACATCTTACAT 796
Qy      718 CAAAGAAATTCATATCGGGAGAGCCCTTACGATGTAAGACTGTGGAGAGGCTTTGCA 777
Db      797 CAGAGAAATTCATATCGTGTGAAGAACCTTATGAATGTAAGAAATGTGAGAGGCTTTAGT 856
Qy      778 TGGGGCTCAAGCTGCTTATTCATTAAGAGATTCATCTGTGTGAAAGAAACCTTATGAAT 837
Db      857 CGTGGCTATCACCTTCTCAGATCAGAAATTCATCTGTGTGAGAAACCTTTTGAATGT 916
Qy      838 AAGAGCTGTGAAGAGGCTTTGCGGTGTGATGAGCTCACTCAGACAGAGATTCAC 897
Db      917 AAGGAATGTGGAGAGGCTTTTGTGGGTTCAGAGCTTGTAAACATGAGAGATTCAT 976
Qy      898 ACTGGGAGAGAAAGCTTACGAAATGCAAGACTGTGGAGAGCCTTTAGCCGTGTATAA 957
Db      977 ACTGGTGAAGAAATCCCATGATGAAGATGAGAGAGGAGGAGGCTTTGTGTGGGTATCAA 1036
Qy      958 CTATTCAGACAGAGAAATTCATTAAGTGGGAGAGGCTTTAGAGTGTAAAGACTGTGG 1017
Db      1037 CTTACTCGACATCAGGATATTTCACTGTGTGAAGAACCTTATGAAGATGTAAGATGTGG 1096
Qy      1018 AAGGCTTTATTTGTGGTCAAGGCTCATTCAGCATAAAGAAATTCACAGGTGAGAA 1077
Db      1097 AAGGCTTTATTTGTGATCAAGGCTTTTTCATGATGAAGAAATTCATACAGGGAGGAA 1156
Qy      1078 CCTATGAATGTCAGAAATGTGGAGAGGCTTTTACTCGAGTCAATTAACCTTACTCAGAT 1137
Db      1157 CCTATGAATGTAAGAAATGTGGAGAGGCTTTTATGCGTATCACCTTACTCAACAT 1216
Qy      1138 CAGAGATCACAAGGCTGTGAAGGCTTCACGAAATGTAAGAGTGTGGAGAGGCTTTGCG 1197
Db      1217 CAGAAATTCATATCCGTGTGAAGACCTTCAATGTAAGAAATGTGGAGAGGCTTCAAGT 1276
Qy      1198 TGGGGTTCAGAGCTGTGTAAGACAGAGAGATCATATCGGGGAGAGGCTTCAAGTGC 1257
Db      1277 TGGGGTTCAGAGCTGTAAGACAGAGAGATCATATGTAAGAGTCTTATGATGT 1336

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OM nucleic - nucleic search, using sw model

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(without alignments)
9628.459 Million cell updates/sec

Title: US-10-111-257-3

Perfect score: 2015
Sequence: 1 cgcctcgcaccggtgacgc.....gtgaagttcctaactaa 2015

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397.8	69.4	1429	3	US-09-023-655-689
2	703	34.9	2143	3	US-09-881-578A-3
3	520.6	25.8	2274	3	US-09-620-312D-154
4	510	25.3	2499	3	US-09-774-528-331
5	502.8	25.0	3472	3	US-10-104-047-415
6	495.4	24.6	1694	3	US-10-104-047-1500
7	478.2	23.7	2925	3	US-09-620-312D-163
8	474.8	23.6	2241	3	US-10-104-047-693
9	461.6	22.9	1914	3	US-10-104-047-1464
10	460.6	22.9	3798	3	US-09-949-016-4204
11	460.6	22.9	156942	3	US-09-949-016-12227
12	460.6	22.9	156850	3	US-09-949-016-15946
13	460.6	22.9	156850	3	US-09-949-016-15946
14	456.6	22.7	2669	3	US-10-104-047-271
15	455.2	22.6	3839	3	US-09-949-016-485
16	451.2	22.4	2666	3	US-09-881-578A-1
17	446.2	22.1	2441	3	US-09-949-016-2756
18	446.2	22.1	19861	3	US-09-949-016-14498
19	445.4	22.1	2320	3	US-09-016-434-1054
20	445	22.1	2660	3	US-10-104-047-559
21	444.6	22.1	3078	3	US-10-104-047-622
22	437	21.7	2978	3	US-09-949-016-3823
23	436.6	21.7	45138	3	US-09-949-016-13027
24	433.6	21.5	3400	3	US-09-799-451-136

25	428.4	21.3	3138	3	US-10-104-047-83	Sequence 83, App1
26	422.8	21.0	2110	3	US-10-104-047-1778	Sequence 1778, App
27	422	20.9	15632	3	US-09-949-016-15565	Sequence 15565, A
28	418	20.7	2625	3	US-10-104-047-1026	Sequence 1026, App
29	416.6	20.7	2351	3	US-09-016-434-1337	Sequence 1337, App
30	416.6	20.7	2637	3	US-09-949-016-5623	Sequence 5623, App
31	416.6	20.7	27227	3	US-09-949-016-17365	Sequence 17365, A
32	415.2	20.6	2752	3	US-09-949-016-3563	Sequence 3563, App
33	415.2	20.6	18824	3	US-09-949-016-15305	Sequence 15305, A
34	412.6	20.5	3026	3	US-10-104-047-967	Sequence 967, App
35	410.4	20.4	1629	3	US-09-016-434-1336	Sequence 1336, App
36	407.2	20.2	1812	3	US-09-016-434-1407	Sequence 1407, App
37	403.4	20.0	128779	3	US-09-497-855A-38	Sequence 38, App1
38	403	20.0	3090	3	US-10-104-047-191	Sequence 191, App
39	402.6	20.0	2357	3	US-10-104-047-1701	Sequence 1701, App
40	400.2	19.9	2798	3	US-10-104-047-371	Sequence 371, App
41	400	19.9	3400	3	US-10-104-047-1037	Sequence 1037, App
42	397.6	19.7	2489	3	US-09-774-528-280	Sequence 280, App
43	397.6	19.7	2489	3	US-10-120-988-280	Sequence 280, App
44	397.6	19.7	2582	3	US-09-016-434-1399	Sequence 1399, App
45	396.6	19.7	2141	3	US-10-104-047-600	Sequence 600, App

ALIGNMENTS

RESULT 1
US-09-023-655-689
Sequence 689, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 689:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TLYNMOT02
CLONE: 450088

US-09-023-655-689

Query Match 69.4%; Score 1397.8; DB 3; Length 1429;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1411; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

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OY 595 GGGAGAGCCTTATGTCGTGGCTATCAACTTACTGACATCAGAAAAATCCATACTGTGAG 654
Db 10 GGGAGAGCCTTATGTCGTGGCTATCAACTTACTGACATCAGAAAAATCCATACTGTGAG 69
OY 655 AAACCTTATGATGTAAGAAATGTAAGAGGCTTCCGTGGGGCAATAGCTTACTCA 714
Db 70 AAACCTTATGATGTAAGAAATGTAAGAGGCTTCCGTGGGGCAATAGCTTACTCA 129
OY 715 CATCAAAAAATCATACTGGGGGAAAGCCCTAGCAATGTAAAGACTGTGGG--AAGGCTT 772
Db 130 CATCAAAAAATCATACTGGGGGAAAGCCCTAGCAATGTAAAGACTGTGGGGAAAGGCTT 189
OY 773 TTGATGGGGCTCAAGCCTCGTTATTCATAGAGATTCATAGTGTGAAAAACCTATG 832
Db 190 TTGATGGGGCTCAAGCCTCGTTATTCATAGAGATTCATAGTGTGAAAAACCTATG 249
OY 833 AATGTAAAGACTGTGAAAGGCTTTGGCGTGTGTATGAGCTCACTCAGCACAGAGAT 892
Db 250 AATGTAAAGACTGTGAAAGGCTTTGGCGTGTGTATGAGCTCACTCAGCACAGAGAT 309
OY 893 TCACACCTGGGGGAAAGACTAGCAATGTCAAGACTGTGGGAAAGACTTTAGCCGTGT 952
Db 310 TCACACCTGGGGGAAAGAGNTACGAATGTCAAGACTGTGGGAAAGACTTTAGCCGTGT 369
OY 953 ATAACTTATTCAGCAAGAGAAATTCATAGTGGGGAAAGCCTTACGAATGTAAGACT 1012
Db 370 ATAACTTATTCAGCAAGAGAAATTCATAGTGGGGAAAGCCTTACGAATGTAAGACT 429
OY 1013 GTGGGAAGCCTTATTTGTGTGTCAAGCCTCTTACAGATAAAGAAATTCACAGAGTG 1072
Db 430 GTGGGAAGCCTTATTTGTGTGTGTCAAGCCTCTTACAGATAAAGAAATTCACAGAGTG 489
OY 1073 AGAAACCTATGTAATGTCAAGAAATGTGGGAAGGCTTTACTCGAGTCAATTAACCTACTC 1132
Db 490 AGAAACCTATGTAATGTCAAGAAATGTGGGAAGGCTTTACTCGAGTCAATTAACCTACTC 549
OY 1133 AGCATCAAGAGATCCACACCGGTGAGAGCCTTCAGAAATGTAAAGGTGTGGGAAGGCTT 1192
Db 550 AGCATCAAGAGATCCACACCGGTGAGAGCCTTCAGAAATGTAAAGGTGTGGGAAGGCTT 609
OY 1193 TTGCGTGGGGTTCGAGCCTTCGTTAAGCAGAGAGATACATAGGGCGAGAAAGCCTTACA 1252
Db 610 TTGCGTGGGGTTCGAGCCTTCGTTAAGCAGAGAGATACATAGGGCGAGAAAGCCTTACA 669
OY 1253 AGTGCACAGAAATGTGGGAAGGCTTCAATTTGTGGCTATCACTCAGCAGAGAGAA 1312
Db 670 AGTGCACAGAAATGTGGGAAGGCTTCAATTTGTGGCTATCACTCAGCAGAGAGAA 729
OY 1313 TCCACACAGAGCCAAACCCCGTATTAATGTAAAGAGTGTGGGAAGGCTTTCATTTATGAT 1372
Db 730 TCCACACAGAGCCAAACCCCGTATTAATGTAAAGAGTGTGGGAAGGCTTTCATTTATGAT 789
OY 1373 CGAGCCTCGTGAACAATGAGAAATTCATACCGGGGTGAAGAAACCTTATGGTGTACGAAT 1432
Db 790 CGAGCCTCGTGAACAATGAGAAATTCATACCGGGGTGAAGAAACCTTATGGTGTACGAAT 849
OY 1433 GTGGGAAGAGCTTATGTCAGGCGCATCAGCTTACAAACATCAGAAAAAGCAGAGGGG 1492
Db 850 GTGGGAAGAGCTTATGTCAGGCGCATCAGCTTACAAACATCAGAAAAAGCAGAGGGG 909
OY 1493 CGAAATCTTACGAATGTAAAGAGTGTGGGAAGGAGCATGTAAACAATTAAACATCTCCGAG 1552
Db 910 CGAAATCTTACGAATGTAAAGAGTGTGGGAAGGAGCATGTAAACAATTAAACATCTCCGAG 969
OY 1553 AACATCAGAGGATCCACACAGTGTGAAGAGCCTTTTGAAGCAGATAGCCGCTCGATCT 1612
Db 970 AACATCAGAGGATCCACACAGTGTGAAGAGCCTTTTGAAGCAGATAGCCGCTCGATCT 1029

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Query Match 34.9%; Score 703; DB 3; Length 2143;
 Best Local Similarity 69.7%; Pred. No. 1,2e-212;
 Matches 1006; Conservative 0; Mismatches 410; Indels 27; Gaps 3;

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OY 1613 ATGTTTGCCTTCCACAGTTTGTATCCTGCGAGTCAGATTCAGAAATATTTAAATG 1672
Db 1030 ATGTTTGCCTTCCACAGTTTGTATCTGACAGTCAATGAGGTTCAAAAAATATTTAAATG 1089
OY 1673 GAAAATTCAGAAATTAAGAAATTTTAAATGTTCAAAATGTGTGCTTCTGAGTACCGTGA 1732
Db 1090 GAAAATTCAGAAATTAAGAAATTTTAAATGTTCAAAATGTGTGCTTCTGAGTACCGTGA 1149
OY 1733 TGAATTCCTGCTGCTCCGCTCCAGCCGCGGGGATGTGAGTATCATCCCTTGTGTACAGC 1792
Db 1150 TGAATTCCTGCTGCTCCGCTCCAGCCGCGGGGATGTGAGTATCATCCCTTGTGTACAGC 1209
OY 1793 ACATCAAGCTGTATATCCAGCCACCCACCTGTAGTACTGATAGTACCGCTTTGTGATCA 1852
Db 1210 ACATCAAGCTGTATATCCAGCCACCCACCTGTAGTACTGATAGTACCGCTTTGTGATCA 1269
OY 1853 GATCAACTATCCAGCATCAAGTGTGCTGTGCTCCCAAGTATGCTTCACTTGTCTTAAAGT 1912
Db 1270 GATCAACTATCCAGCATCAAGTGTGCTGTGCTCCCAAGTATGCTTCACTTGTCTTAAAGT 1329
OY 1913 GGCCCGAGAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1972
Db 1330 GGCCCGAGAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1389
OY 1973 AGTGCTTCCTTTTAAATGAAAAAGTGAAGTTCTCACTT 2012
Db 1390 AGTGCTTCCTTTTAAATGAAAAAGTGAAGTCTCACTT 1429

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RESULT 2
 US-09-881-578A-3
 ; Sequence 3, Application US/09881578A
 ; Patent No. 6596855
 ; GENERAL INFORMATION:
 ; APPLICANT: Hering, Thomas M.
 ; APPLICANT: Johnstone, Brian
 ; TITLE OF INVENTION: PROBES FOR CHONDROGENESIS
 ; FILE REFERENCE: 27708/04013
 ; CURRENT APPLICATION NUMBER: US/09/881,578A
 ; CURRENT FILING DATE: 2001-06-14
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 2143
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-881-578A-3


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OY 448 AGCTTGAAGAACCAAGCGCTCCAGAGGAGGTATGTCATCAGATGATCATTTAT 507
DB 310 ATATTGAGGGACTTAAAGACATCAAGGGATCTTACGTCATGATTAATTCAGCTAT 369
OY 508 GTCAAAAGGCGCTGCTACTAGAGAGCACCCCTCTAGAACATCAGAGA---CATCAT 564
DB 370 GAAAAAATATCTTTACAGAAAAAGTAAATCTTTACTCCATCAAGAAATTCATTAAT 429
OY 565 AAGGGAATTCCTTTGATGTAAAGACTGTGGGAAGGCTTTAGTCGTGCTATCACTT 624
DB 430 ACAGAGAAATCCTATGTTGTGAAGAAATGTGGAAAGGCTTGCATGCTCAAAACTT 489
OY 625 AGTCAACATCAGAAATCATCTGCTGAGAAACCTTATGAATGTAAAGATGAAGAAG 684
DB 490 GTTCAACATGAGAAATCTATCAGCTGAAAGCACTTGAATGTAAAGAAATGGGAAG 549
OY 685 GCGTTCGTTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTGGGAGAACCC 744
DB 550 AATTATTTAAGTCCATCATCAATGTCAGAGATTTCAATCTGTGAGAAACCC 609
OY 745 TACGATGTAAAGACTGTGGGAAGGCTTTTCATGGGCTCAAGCCTGTTATTCATAG 804
DB 610 TATGAGTGAAGAAATGTGGGAAGACCTTTAGCTGGGATCAAGCCTGTAAACATGAG 669
OY 805 AGGATTCATCTGAGAAAAACCTATGAAATGTAAAGACTGTGAAAGGCTTTGGGCGT 864
DB 670 AGAATTCACATCTGTGAGAAACCTATGATGTAAAGAAATGTGGGAAGGCTTTAGTGT 729
OY 865 GGTGATGAGCTCACTCAGACCCAGAGATTCACACTGGGGAGAAAGACTACGATCAAA 924
DB 720 GGCCTTCACTTACCAACATCAGAAAAATTCATATTGGTGAATCTTATAAGTAAAG 789
OY 925 GACTGTGGGAAGACTTTAGCCGTGTATAAATTATTCAGCAAGAGAAATTCATAGT 984
DB 790 GAATGTGGGAAGGCTTTTGTGGGCTCAAGCCTTGCTAAACATGAGATTAATTCATCA 849
OY 985 GGGGGAAGGCTTACGAGTGTAAAGACTGTGGGAAGGCTTTATTTGTGCTCAAGCCTC 1044
DB 850 GGTGGAAGGCTTTATTAATGTAAAGAAATGTGGGAAGGCTTCACTGTGCTATCACTT 909
OY 1045 ATTACAGATTAAGAAATTCACAGAGTGAAGAACCTTATGAATGTCAAGAAATGTGGAG 1104
DB 910 ACTCAGATCAGAAAAATCATCTGCTGTAAAGAAACCTTATGAATGTAAATATGTGAAAG 969
OY 1105 GCCTTTACTCGAGTCAATTACTTACTCAGCATCAGAGATTCACACCGGTGAGAACCTT 1164
DB 970 GCTTTTGTGGGCTATCACTTACTCGACATCAGATTTTCATATCTGTGAGAAACCC 1029
OY 1165 CACGAATGTAAAGAGTGTGGGAAGGCTTTGCTGGGGTTCAGGCTGTGAAGACGAG 1224
DB 1030 TATGATGCAAGAAATGTGGGAAGGCTTTAATTTGGGATCAAGCTTATTCACACTGAA 1089
OY 1225 AGGATACATACGGGCGAGAGGCCGTACAGTGACAGAGATGTGGGAAGGCTTCAATTGT 1284
DB 1090 AGAATTCATACGTGTGAGAAACCTTATGAATGTAAAGAAATGTGAAAGGCTTTAGTGT 1149
OY 1285 GGCCTTACCTCAGCAGCAGAGAGATTCACACAGCGGAAACCCCGTATTAATGTGAAG 1344
DB 1150 GGCCTTACCTTTTCCAAATCAGAAATTCATCTGTGAGAAACCTTTTAAATGTGAAG 1209
OY 1345 GAGTGTGGGAAGGCTTTCATTTATGATGAGCTCGTGAACATGAGAGATTCATACC 1404
DB 1210 GAATGTGGGAAGGCTTTTATGTTGGGTTCAAGCCTTTTAAACATGAGAGATTCATAC 1269
OY 1405 GGGGTGAACCTTATGGGTGTACAGAAATGTGGAAAGGCTTTTATGTCACGGCCATCAGCTT 1464
DB 1270 GGTGAGAAATCCCATGAATGTAAAGAAATCGGAAAGACCTTTTGTAGTGGATCAACTT 1329
OY 1465 ACACAAATCAGAAAAAGCAGCTGTGGGGAATCTTACGATGTAAAGAGTGTGGGAAG 1524
DB 1330 ACTCAGACATCAGGTATTTTCACTGTGTGAAAGCCCTTATGAATGTAAAGAAATGTGGGAAG 1389
OY 1525 GCATGTAAACCACTTAACCATCTCGAAGAACATCAGAGGATCCACAAACGTTGAAGAGCC 1584

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DB 1390 GCTTTAATTTGTGATCAAGCTTTGTTCAACATGAAAGAAATTCATACAGGGAGAAACCC 1449
OY 1585 TTT 1587
DB 1450 TAT 1452

RESULT 3
US-09-620-312D-154
; Sequence 154, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 154
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(460)
; US-09-620-312D-154

Query Match 25.8%; Score 520.6; DB 3; Length 2274;
Best Local Similarity 63.1%; Pred. No. 1.4e-154;
Matches 930; Conservative 0; Mismatches 509; Indels 34; Gaps 7;

OY 121 CTCCTGGAATTTGCTCTTCAAGTGAAGAACCCGGAAGACATGATCAGTTCTCAGTCT 180
DB 56 CTCCTGACTTTCACACCTCCAGAGAAAGAACCCGAAATTTGATCAAGTTC-----TAA 109
OY 181 AAAACAATGAGCCAGAGGTTTGTGACGTTTGGCCGACGTAGCCATAGACTTTTTCAGAGAG 240
DB 110 AAAACATAGCCCACTTTGTGTGACTTTTCAAGGAGATGTGGCATTTGACTTCTCAGAGAG 169
OY 241 GAGTGGGCGCTGTCTGAATCTGTCTCAGAGGGAAGCTGTACTGGGACGTGATGCTGAGAAAC 300
DB 170 GAATGGGAATGCTGGAGCCCTGCTCAGAGGGAAGCTGTACAGGAGATGATGTGTGAGAAAC 229
OY 301 TACAGTAACCTTGATCTCACTGGAATTTGGAGTCAGCATATGAAAAATGAAGTTTACTCTCA 360
DB 220 TACAGCAACCTGATCTCATTTGACCTTGAATTCAGTGTGTGACCAAAAAAGTTATCTCCA 289
OY 361 GAAAAAAACATTCATGAATAAGAGGCTTCCAAAAGAAATTCAGATGAAGAAAT----- 414
DB 290 GAAAAAGAAATTTATGAATGAATGAAATCACTCCAGTGGGAGAAATATATGGGAAACGTATCAAC 349

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QY 415 -----AAATCCCTTGCCGCTAATGATATGGAAGTACGCTTGAAG 458
Db 350 CATCACCTTTCAATACATAGTGTCTTGAAACAAATATGAGTGCAGAAAGCACTTAAAGG 409
QY 459 ACCACAGCGCTCCAGAGGAGGTATGCAATGATGATCATCAATTAATGTCAAAAGGCC 518
Db 410 TCAAGTAAGCAAGTCAAGAGGGGCTTACATGTGTGTCAAAATTAACCTGTGAAGAAAAGGC 469
QY 519 TCGTACTAAGAAAGGCAACCCCTCTGTGAACAATCAGAGACATCAT--AGAGAAATTCG 576
Db 470 CACTGAAGTCAATTCACCTCTTCTAATTCATCGAATTAATCCATACCAAGGAAAAAT 529
QY 577 TTTGAATGTAAGAGCTGTGGGAAAGCCCTTATGCTGTGCTATCACTTATGTCAATCAG 636
Db 530 GTCAAAATGTAAAGAAATGCAAGAGTTTCACTGCTGATCCTGATCCTTATTCACATGAG 589
QY 637 AAAATCCATACGTGTGAGAAACCTTATGATGTAAGAAATGTAAAGAGGCTTCCGTTGG 696
Db 590 GAAATCATATATATATATAAAATGCTCTGAAGTTAATTAACAAGAAATCCTTTAGCAAA 649
QY 697 GGCAATCAGCTTACTCAACATCAAAAAATTCATCTGGG--GAGAAGCCCTAGCAATGTAA 755
Db 650 AAGCCAAAGCTATATTTTAACATCAAGAAATTCAGACTGGGTGAGAAACCTTATGAGTAT 709
QY 756 AGACTGTGGGAAAGGCTTTTCATGATGGGGCTCAAGCCTGTTATTCATTAAGAGATTCATAC 815
Db 710 GGAATGTGAAAGAGCCCTTGTGTGTACTTGTACTTCATTCATCAACATCAAGAAATTCATAC 769
QY 816 TGGTGAAGAAACCTTATGAATGTAAAGACTGTGAAAGGCCCTTTCGCGGTGTATGATAGCT 875
Db 770 TTAATGAAAAACCTTATCAAGTGAAGCATGTGGGAAAGCTTTTATTCGTGTGTACAGCT 829
QY 876 CACTGACACAGAGATTCACACTGGGGGAAAGACTAGATGCAAGAACTGTGGAA 935
Db 830 CACTGAACATCAAGAGGTTCAACAGAGAGAAACCATATGATGTAAAGAAATGTGAAA 889
QY 936 GACCTTTAGCCGCTGTATTAACCTTATTCAGACAAGAGAAATCATAGTGGGAGAGCC 995
Db 890 AGCTTTAGTAT--TGTCAACAATATCTCTTCATCAGAGAAATCATAGTGTGAAAAAC 948
QY 996 TTAAGAGTGAAGACTGTGGGAAAGCTTTTATTTGTGTGTCAAGCCTCATTCAGATTA 1055
Db 949 CTAATGATGT--AAGATTTGTGGAAAGGCCCTTATCT--TGGCTCTCAACTTACTTACATCA 1006
QY 1056 AAGAATTCACAGGTGAGAAACCTTATGATGTCAAGAAATGTGGGAAAGGCCCTTACTCG 1115
Db 1007 GAGAAATTCATAGTGTGAGAAACCTTATGATGTGAAGAAATGTGGAAAGGCCCTTATCT 1066
QY 1116 AGTCAATTAACCTTACTCAGCATGAGAAATTCACACCGGTGAGAGGCCCTCAGCAATGTAA 1175
Db 1067 TGGTTCACACCTTACATACATCAGAGAGTTCACTAGTGTGAAAGGCCCTTACATATGTAA 1126
QY 1176 GGAAGTGGGAAAGGCCCTTGTGCTGTGGGTTGAGCCTTGTTAAGCAGAGAGATACATAC 1235
Db 1127 AGAATGTGGGAAAGGCCCTTTTATGTGCTCCAACTGAATGAACATCAGAGAAATTCATAC 1186
QY 1236 GGGCGAGAGGCCCTTACAGTGCACAGAAATGTGGGAGGCCCTTCAATTTGTGGCTATCACCT 1295
Db 1187 AGAGAGGAAACCTTATGAATGTAAAGAAATCGGGGAAACCTTTTGTGTGCTCAACAAT 1246
QY 1296 CACTCAGCAGAGAAATTCACACAGGCGAAACCCCTATTAATGTAAAGAGTGTGGAA 1355
Db 1247 TACTTACACCTGAGAGTTCACTCAGTGAAGAGCTTATTAATGCAAAAGAAATGTGGAA 1306
QY 1356 GAGCTTCATTTATGATGAGAGCCTGTGAAACATGAGAGAAATTCATACCGGGGTGAAGCC 1415
Db 1307 AGCCTTATTTCTAATCTAATCTTATTCACATCAAGAAATTCATACCGGAGAGAGGCC 1366
QY 1416 CTATGGGTGACAGAAATGTGGGAAAGCTTTAGTACAGGCGCATAGCTTACAAACATCA 1475
Db 1367 CTACAAATGTAAAGAAATGTGAAAGGCCCTTTATTTGTGCAAAACACTTATGTGAACATCA 1426

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QY 1476 GAAAAAGCAGAGTGGGGGGAATCTCAAGAAATGTAAGAGTGTGGGAAAGCATGTAAACA 1535
Db 1427 GAGAAATTCATACAGGTGAGAAACCTTTGAATGTAAAGAAATGTGAAAGGCCCTTATTCG 1486
QY 1536 CCTAAACCATCTCCAGAGAAATCAGAGGATCCA 1568
Db 1487 TGTTCATATCTTACTCAACATGAGAAAAATTCATCA 1519

RESULT 4
US-09-774-528-331
; Sequence 331, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 331
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (222)..(1820)
; US-09-774-528-331

Query Match      25.3%; Score 510; DB 3; Length 2499;
Best Local Similarity 63.6%; Pred. No. 3.6e-151;
Matches 821; Conservative 0; Mismatches 445; Indels 24; Gaps 2;

QY 322 GATTTGAGTCAAGCATATGAAAAATTAAGCTTTACTTACAGAAAAAAATTCATGAAATA 381
Db 450 GATTGGAAGCCAAAGTATGAGACCAAGAAATTTATCTTTAGAAAAATGACATTTATGAAATA 509
QY 382 AGGGCTTCCAAAAGAAATTCAGTAGAAGAAATTCCTTGGCCGTAAAC----- 432
Db 510 AATTATCCCAAGTGAAGTAATGAAAGAAATGGAACCAATGAGCTTTAAGGCTCAT 569
QY 433 -----TGATATGTGAAGGTAGCGCTTGAAGAACACAGGCGTCCAGAGGAGG 480
Db 570 TTAATAAATGATTTGGAAATCCACAGAAAAATTTGAAGACAGAGAGACTCAAGAAAGA 629
QY 481 TATGTCAATCAGATGATCATCAATTAATGTCAAAAGGCCCTGTACTAGAGAGGACCCCT 540
Db 630 TACTTCAAGTATGTGAAATGAGCATCTGAAGAGGTCTCTTACCAAGAAACGACATCT 689
QY 541 CTTAGAACATATAGAGATCA--TAAAGAAATTCCTTTGAATGTAAAGAGCTGTGG 597
Db 690 GTTACTCCACATAGAGACTTCAATTTGTGATTAACCTTATGAATGTAAAGAGATGTGG 749
QY 598 AAGGCTTTAGTGTGCTATCAACTTATGCAATCAGAAATTCATCTGTGTGAGAA 657
Db 750 AAGGCGTTCAAGATGTGGCGCAAGCTTACTTTTCAATCAAGAAATTCATCTGTGTGAGAA 809
QY 658 CTTATGAATGTAAAGAAATGTAAAGAGGCCCTTCGTTGGGCAATCAGCTTACTCAACAT 717

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Db      810 CCGTATGATGTAAAGAAATGTGGATGGCTTTCAGACAGACTGCACACTTACTGCACAT 869
Qy      718 CAAAAATTCATACCTGCGGAGAAAGCCCTACGAATGTAAAGACTGTGGAAAGCCCTTTCGA 777
Db      870 CAGAGACTTCATCTGTGTGTAAGAACTCTATGATGTAAAGAAATGTGGGAAAGCTTTCATA 929
Qy      778 TGGGGCTCAAGCTCTGTTATTCATTAAGAGATTCATCTGTGTGTAAGAAAGCCCTATGATGT 837
Db      930 TGTGTGACAGATCTTAAGATACATCAGAAATGCAATTTGTGTGTAAGAAAGCCCTATGATGT 989
Qy      838 AAAGACTGTGAAAGCCCTTTCGCGGTGTGTAGTCACTCAGACACAGATTCACAG 897
Db      990 AAAGATGTGGAAAGCCCTTTCAGGATCAGAGACAACTTACTCTGCATCAGAGATTCAT 1049
Qy      898 ACTGGGAGAAAGACTACGAATGCAGAAAGCTGTGGAAAGCCCTTTCAGCGGTGTATATA 957
Db      1050 ACTGTGTGAAAGCCCTATGTGTGTAAAGGTGTGAAAGCCCTTTCAGACGTATCGACAC 1109
Qy      958 CTTATTCAGACACAAAGAAATTCATAGTGGGAGAAAGCCCTTTCAGAGTGTAAAGCTGTGG 1017
Db      1110 CTGACTCGGCATCAGAAAGCTTAATGTGTGACAGGCTCTATGAAATGCAGAAAGATGTGG 1169
Qy      1018 AAGGCTTTATTTGTGTTCAGAGCCCTTTCAGCANTAAAGAAATTCACACAGGTGAGAA 1077
Db      1170 AAGGCTTTTGTGTGTCTGTGTCTTGTAGATACATCAAACTTCATCTGTGTGAGAA 1229
Qy      1078 CCTATGATGTCAAGAAATGTGGAAAGCCCTTTCAGTCAATTCCTTTCAGCAT 1137
Db      1230 CCTATGATGTAAAGAAATGTGGAAAGCCCTTTCAGTGTGCAACAACTTCATCTCCAT 1289
Qy      1138 CAGAAATTCACACCGGTGAGAAAGCCCTCAGAAATGTAAAGAGTGTGGAAAGCCCTTTCGC 1197
Db      1230 CAGAAATTCATATCTGTGTGAGAAAGCCCTTGTAAATGTAAAGAAATGTGAAAGACCTTTAGC 1349
Qy      1138 TGGGGTGTGAGCCGTGTAAAGACGAGATACATAGCGGGGAGAAAGCCGTAAAGAGTGC 1257
Db      1350 CTTGTGTATCATCTTATCTTCATCAACAAATTCATCTGTGTGAAAGCCCTTTCAGATGT 1409
Qy      1258 ACAGAAATGTGGAAAGCCCTTTCATTTGTGTCTATCACTCTCAGACAGAGAAATTCAC 1317
Db      1410 AAGGAATGTGAAAGCCCTTTCATGTGTCTATCACAACCTTATTCATCTCAGAGATTCAT 1469
Qy      1318 ACAGGCGAAAGCCCTTATTAATGTAAAGAGTGTGGAAAGCCCTTTCATTTATGATGAGC 1377
Db      1470 ATTGTGTGTAAAGCCCTTATGATGTAAAGAGTGTGGAAAGCCCTTTCAGACTTTCACAA 1529
Qy      1378 CTTGTGAAACATGAGAAATTCATACCGGGGTGAAAGCCCTATGGGTATCAGAAATGTGG 1437
Db      1530 CTCACACAGCATCAGATGTATCTATTTGTGTGAAAGCCCTTATTAATGTAAAGAAATGTGGC 1589
Qy      1438 AAGACTTTAGTACAGGCGCATCAGCTTACACAACATCAGAAAGCGCAGTGGGGGAGAA 1497
Db      1590 AAGGCTTTTATGATGTGGCCAAAACCTTACTTACATCAGAGATTCATCTGTGGCGAGAA 1649
Qy      1498 TCTTACGAATGTAAAGAGTGTGGGAAAGCATGTAAACCATTAACCATTCCTGAGAAAT 1557
Db      1650 CCTTTGAGTGTAAAGAAATGTAGAAAGCCCTTTCAGCTTAATTCATCTCTTATTCACAT 1709
Qy      1558 CAGAGATTCACACAGCTTGAAGAGCCCTT 1587
Db      1710 CTGAGAAATTCATTTGTGTGAGAAACCTTAT 1739

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RESULT 5
US-10-120-988-331
; Sequence 331, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenshua
; APPLICANT: Ren, Feiyun

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; APPLICANT: Wang, Dunhui
; APPLICANT: Drenth, Radoje T.
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 331
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (222)..(1820)
US-10-120-988-331

Query Match      25.3%; Score 510; DB 3; Length 2499;
Best Local Similarity 63.6%; Pred. No. 3.6e-151;
Matches 821; Conservative 0; Mismatches 445; Indels 24; Gaps 2;

Qy      322 GATTGTGATCAGCATATGAAATTAAGACTTACTTACAGAAAGAAACATTCATGAAATA 381
Db      450 GATTGTGAGACCAAGATAGACCAAGAAATTTAGAAATGACATTTATGAAATA 509
Qy      382 AGGCTTCGAAAGAAATTCAGATGAAAGATTAATCCCTTGGCCGTAAAC----- 432
Db      510 AATTATCCAGTGAAGATTAAGAAAGATTTGAAACCATGCTTAAAGGTCTCAT 569
Qy      433 -----TGAATATGTGAAGTACGCTTGAAGACCAAGCGCTCAGAGGAGG 480
Db      570 TTAATAAATGATTTGGAATCCACAGAAATTTGAAGACAGAGAGACTTCAGAAAGGA 629
Qy      481 TATGTCAATCAGATATATCATTAATGTCAAAAGCCGTCTACTAGAGAAAGCAACCT 540
Db      630 TACTTCAGTGTGTAAGAAATGCAATCTGAAAGGTGTCTCTTTCAGAAAGCAATCT 689
Qy      541 CCTAGAACATCAGAGACATCA---TAAGGAAATTCCTTGAATGTAAAGACTGTGG 597
Db      690 GTTACTCCACATCAGAGACTTCTTTGTGTATTAACCTTATGAAATGTAAAGAAATGTGG 749
Qy      598 AAGGCTTTTATGTGTGTATCACTTATGATCAATCAGAAATTCATCTGTGAGAA 657
Db      750 AAGGCTTTCAGAGTGCAGCAAGCTTCTTTCATCAGAAATTCATCTGTGAGAA 809
Qy      658 CTTATGAAATGTAAAGATGTAAAGAGCCCTTCCGTGGGCAATCAGCTTACTCAACT 717
Db      810 CCGTATGAAATGTAAAGATGTGGAGTGCCTTTCAGACAGACTGCACACCTTACTGCACAT 869
Qy      718 CAAAAATTCATACCTGCGGAGAAAGCCCTACGAATGTAAAGACTGTGGAAAGCCCTTTCGA 777
Db      870 CAGAGACTTCATCTGTGTGTAAGAACTCTATGATGTAAAGAAATGTGGGAAAGCTTTCATA 929
Qy      778 TGGGGCTCAAGCTCTGTTATTCATTAAGAGATTCATCTGTGTGTAAGAAAGCCCTATGATGT 837
Db      930 TGTGTGACAGATCTTAAGATACATCAGAAATGCAATTTGTGTGTAAGAAAGCCCTATGATGT 989
Qy      838 AAAGACTGTGAAAGCCCTTTCGCGGTGTGTAGTCACTCAGACACAGATTCACAG 897
Db      990 AAAGATGTGGAAAGCCCTTTCAGGATCAGAGACAACTTACTCTGCATCAGAGATTCAT 1049
Qy      898 ACTGGGAGAAAGACTACGAATGCAGAAAGCTGTGGAAAGCCCTTTCAGCGGTGTATATA 957
Db      1050 ACTGTGTGAAAGCCCTATGTGTGTAAAGGTGTGAAAGCCCTTTCAGACGTATCGACAC 1109
Qy      958 CTTATTCAGACACAAAGAAATTCATAGTGGGAGAAAGCCCTTTCAGAGTGTAAAGCTGTGG 1017
Db      1110 CTGACTCGGCATCAGAAAGCTTAATGTGTGTGACAGGCTCTATGAAATGCAGAAAGATGTGG 1169
Qy      1018 AAGGCTTTTATTTGTGTTCAGAGCCCTTTCAGCANTAAAGAAATTCACACAGGTGAGAA 1077

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Db 1170 AAGGCTTTTGTGTGCTCTGTCTTAAAGTACATCAAACTTACTGTGTGAAA 1229
Qy 1078 CCTATGAATGTCAAGATGTGGAAAGCCTTACTCAGTCAATTAACCTACTCAGAT 1137
Db 1230 CCTATGAATGTCAAGATGTGGAAAGCCTTACTCAGTCAATTAACCTACTCAGAT 1289
Qy 1138 CAGAAATCCACACCCGGTGAAGACCTCAAGATGTGAAGTGTGGAAAGCCTTTCGC 1197
Db 1290 CAGAAATCCATATCTGTGAGAAACCTTATGAATGTGAAGATGTGAAAGACCTTTCGC 1349
Qy 1198 TGGGTTTCAAGCTCTTAAAGCAGAGATATACGGGCGAAGACCTTCAAGTGC 1257
Db 1350 CCGTGTATCATTTATCTTCATCAAGATTCATATCTGTGAAAGACCTTATCGATGT 1409
Qy 1258 ACAGAAATGAGGAGCCTTCAATTTGGCTATCAGCTCAGCAGAGATATCCAC 1317
Db 1410 AAGGAATGCTGGAAGCCTTATGTCTCTACATCACTTATTCATCAGATATTCAT 1469
Qy 1318 ACAGGCGAAACCCGTTATTAATGTGAAGATGTGGAAAGCCTTCAATTAATGATCAGC 1377
Db 1470 ATTTGATTAAGCCTATGATGATGAAGATGTGGAAAGCCTTCAAGATATTCACAA 1529
Qy 1378 CTCTGAATATGAAGATATCTACCGGGGTGAACCTTATGGGTGTACAAATGTGG 1437
Db 1530 CTCACACACATCAGATATTCATATTTGTGAAGAACTTATTAATGTGAAGATGTGC 1589
Qy 1438 AAGAGCTTTAGTCAAGCAGCTTACCAACATCAGAAACGACAGTGGGCGAAA 1497
Db 1590 AAGGCTTTTATGTGGCCCAAACTTATCTTCAATCAGAGCTTATCTGCGCGAAA 1649
Qy 1498 TCTTACGAATGTGAAGATGTGGGAAAGCATGTAAACCACTTAACCTCCGAAACAT 1557
Db 1650 CCTTTAGATGAAGATGTGAAGAGCCTTATGACTTATTCATCCCTTATTCAAACAT 1709
Qy 1558 CAGAGATCCACACAGTTGAAGACCTT 1587
Db 1710 CTGAAGATTCATTTCTGTGAGAAACCTTAT 1739

RESULT 6
US-10-104-047-415
; Sequence 415, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104, 047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 415
; LENGTH: 3472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-415

Query Match 25.0%; Score 502.8; DB 3; Length 3472;
Best Local Similarity 67.0%; Pred. No. 8.8e-149;
Matches 714; Conservative 0; Mismatches 352; Indels 0; Gaps 0;
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Qy 559 CATCATTAAGGAATTCCTTGAATGTAAAGATGTGGAAAGCCTTACTGTGCTAT 618
Db 769 CATACTGGAAGAAACCTTTGAATGTAAAGATGTGGAAAGCCTTTCACATTCATA 828
Qy 619 CAATTAAGTCAATCAGAAATCCATCTGTGAGAAACCTTATGAATGTAAAGATGT 678
Db 829 CAATTAAGTCAATCAGAAATTCATCTGTGAGAAACCTTATGAATGTAAAGATGT 888
Qy 679 AAGAAGCCTTCCGTTGGGCAATCACTTAATCAATCAAAAAATTCATCTGGGAG 738
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Db 889 GGAAGGCTTTATGCTTCTTATCCCTGTATATCCCATTAAGAACTTCAACAGGTGAG 948
Qy 739 AAGCCTTACGAATGTAAAGATGTGGAAAGCCTTTCATGTGGGCTCAAGCCTGTATAT 798
Db 949 AATCTTTGAATGTGAAGATGTGGAAAGCCTTATTCATGTGCTCAAACTTGTTCAA 1008
Qy 799 CATTAAGAGATTCATCTGTGAAAAACCTTATGAATGTAAAGATGTGGAAAGCCTTT 858
Db 1009 CATCAGAGATTCATCTGTGTGTAAGAAACCATATGAATGTGAAGATGTGGAAAGCCTTT 1068
Qy 859 CCGCTGTGTGATGACTCTCAGACAGAGATTCACACTGTGGGAGAAAGCTTATCGAA 918
Db 1069 AATCTGTGTGACACCTTATTAAGCAAAATTCATTCATTAAGAAACCTTGTGA 1128
Qy 919 TCAAAAGATGTGGAAAGCCTTATGCGTGTATTAATCTTATTCAGACAAAGAAAT 978
Db 1129 TGTAAAGATGTGGATGTGCTTGTGATATCATTTACCACTTATTAAGATTCGCAAT 1188
Qy 979 CATATGTGGGAGAGCCTTACAGATGTAAAGATGTGGAGGCTTTATTTGTGTTCA 1038
Db 1189 CATACTGTGTGAGAAACCTTGAATGTAAAGATGTGGAAAGCCTTATCTCTGACAA 1248
Qy 1039 AAGCTTATTCAGATTAAGATTCACACAGGTGAAGACCTTATGAATGTCAAGATGT 1098
Db 1249 AAGCTTGTGCAATCAGAAATTCATCTGTGTGAGAAACCTTGTGAATGACAGGATGT 1308
Qy 1099 GGAAGGCTTTATCTGAGATCAATTAACCTTATCAGATCAGAAAGATCCACCGGTGAG 1158
Db 1309 GGAAGGCTTTATAGTCTTTCACACAGCTTATTCGCAATTAAGAACTTACACAGGTGAA 1368
Qy 1159 AAGCTCAGAAATGTGAAGATGTGGAAAGCCTTTCGTTGGGTTTGAGCCTCTTAAG 1218
Db 1369 AAACCTTTGAATGTGAAGATGTGGAAAGCCTTATATCTGAGCTCAAACTTGTTCAA 1428
Qy 1219 CACGAGAGATCATATCGGCGAGAAAGCCTTACAGATGACAGAAAGTGGAAAGCCTTC 1278
Db 1429 CATCAGAGATTCATGTGTGTATTAAGAAACCATATGAATGTGAAGATGTGGAAAGCCTTT 1488
Qy 1279 AATGTGCTATCACTCACTCAGCAGAGATTCACACAGGCGAAAACCCCGTATTA 1338
Db 1489 AATCTGTGTGACACCTTATTCAGATCAGAAATTCATTCATTAAGAAACCTTTTGTGA 1548
Qy 1339 TGTAAAGATGTGGAAAGCCTTATTAATGAATGAGCCTGTGAAACATGAAGATTT 1398
Db 1549 TGTAGGAATGTGAAGATGTGCTTATGATATCATATGCACTTATTAAGAACTTCCAAAT 1608
Qy 1399 CATACCGGGGTGAACCTTATGTGTATAGAAATGTGGAAAGCCTTATGATCAGGCCAT 1458
Db 1609 CATATGTGTGACAAAGCATTTGAATGTCAAGATGTGGAAAGCCTTCAATCGTGTCTCA 1668
Qy 1459 CAGCTTACACATCAGAAACGACAGTGGGCGAAAATCTTACGAATGTAAAGAGTGC 1518
Db 1669 AGCTTGTTCACATCAGAGATTCACATCTGTGAGAAAGCCTTATTAAGAGATGT 1728
Qy 1519 GGAAGGCAATGTAAACCACTTAACCATCTCCGAGAACATCAGAGATTCACAAACAGTTGA 1578
Db 1729 GGAAGGCTTTTATGACTTATTAACCTTAACCACTTCCCAATCAGAAACTCAGACAGTGA 1788
Qy 1579 AAGAAGCTTTGAACGAGATAGCCGCTGTATATATGTGCTT 1624
Db 1789 AAACCAATTTGAATGTGAAGATGTGGAAATTTCTTCTGTGTGTT 1834
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RESULT 7
US-10-104-047-1500
; Sequence 1500, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104, 047
```

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; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1500
; LENGTH: 1694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1500

Query Match      24.6%; Score 495.4; DB 3; Length 1694;
Best Local Similarity 61.5%; Pred. No. 1,3e-146;
Matches 878; Conservative 0; Mismatches 516; Indels 33; Gaps 4;

QY 182 AAACAATGCCCCAGGGTTGGTGTGACGTTGCCGACGTAGCCATGACCTTTCTCAGAGAG 241
DB 254 AAGCCATGGCTGAGGGATCAGTGTATGTTCAAGTATGTCATAGACTTCTCTCAGAGAG 313
QY 242 AGTGGGCTGTCTGAACTCTGCTCAGAGGACCTGTACTGGGACGTGATGCTGGAGAACT 301
DB 314 AGTGGGACCTGCTGAGACCTGTTCAGAGGGACCTTATACAGAGATGTGATGTTGAGAACT 373
QY 302 ACAGTAACCTTGGTCTCACTG-----ATTGGAGTCAGCATATGAAATAAGATT 353
DB 374 ACGGCAATCTGTTTCAATGGACCTTTACACTCTCAAGCTTCAAGTATCTCTTATTGG 433
QY 354 ACCTACAGAAAAAATTCATCATGAAATAAGGGCTTCCAAAGAAATTCAGATAGAGAG 413
DB 434 AACAGAGAAAGAGCCCTGATGATGTTGGCAGAGACTTACAGAGAGCCGTGTTCAGATC 493
QY 414 TAAATCCCTTGGCCCTAAC-----TGGATATGTGAAGGTACGCTTGAAGACCAAG 465
DB 494 TGGATTCAGATGTGAAAAACAATTATATCTCTAAGAGGAAGATTATGAAATAGAA 553
QY 466 CGCTCCAGAGGGAGGTA-----TGTCATCAGATGATCATCAATTATGCAAAAGGC 517
DB 554 TATGCCAGAGGGAGTAATGGACCTTACAAAGACAGGCCCTTGAGTACTCCAGTTTGGAG 613
QY 518 CTGCTACTAGAGAGAGCAACCCCTCTAGAACACATCAGAGCATATAGAGAAATTCCT 577
DB 614 ATGTTTGGAAATATAGAAAGCCACTTGGAAAACAACTGGGATATCAATGGGGCAATTTTA 673
QY 578 TTGAA-----TGTAAGACTGTGGAGGCCCTTATAGTGTGGCTATCACTTATGTC 628
DB 674 GTCAAGAAATATTCACCTCCTGAATCATGCCACATTTATTCACAGACATTCCTTACTC 733
QY 629 AACATCAGAAAAATTCATCTGTTGAGAAAACCTTATGAATGTAAAGATAGAGAGCCCT 688
DB 734 TCCATCAAAATATTAATATATAGAACAGACCCCTTATGATGTAAAGAAATGTGAAAGCCCT 793
QY 689 TCCGTTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTGGGGAGAGCCCTACG 748
DB 794 TTAGTCAGAACTCACAAATTTATTCACATCAGAAATTCATATGTGTGAAAAATCTTATG 853
QY 749 AATGTAAAGACTGTGGAGAGGCTTTTTCATGGGGCTCAAGCCTGTTATTCATTAAGAGA 808
DB 854 AATGTAAAGAGTGTGGAAATCTTTAGTGTGTTCACATGTTCTCGGCATTCGAAAA 913
QY 809 TTCACTACTGGTGAAGAAACCTTATGAATGTAAAGACGTGGAGAGCCCTTGGCGGTGGTG 868
DB 914 TTCACTACTGGCGAAGAAACCTTTGAATGTAAAGATGTGAGAAAGCCCTTCAGTTGACT 973
QY 869 ATGAGCTCACTGACAGCAGAGATTCACACTGGGAGAGAAAGACTAGAAATGCAAAAGCT 928
DB 974 CATACCTTTCTCAACATCAGAGAAATCCATACCGGTAAAGAAACCTATGAAATGTAAAGAA 1033
QY 929 GTGGGAAAGCCTTTAGCCGTGTGTATAAATCTTATCAGACAGAGAAATTCATATGGGG 988
DB 1034 GTGGGAAAGCCTTTAGTATGTCTCAAAATCTTATGACCATCAGGAAATTCACACTGGG 1093
QY 989 AGAAGCCTTACAGAGTAAAGACTGTGGAGAGCCTTTTATTTGTGTTCAAGCCTCATTC 1048

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DB 1094 AAAAACTTATGAATGTAAAGTATGTGGAGAGCCCTTACTAAGAGCTCACAACTTTTTC 1153
QY 1049 AGCATAAAGAAATTCACACAGGTGAGAAACCTTATGAATGTCAAGAAATGTGGAGGCCCT 1108
DB 1154 AGCATGACGAATTCATCAGGTGAGAAACCTTATGAATGTAAAGAAATGTGGCAAAAGCCT 1213
QY 1109 TTACTGAGTCAATTAACCTTACTGAGCATCAGAGATCACAACCGGTGAGAAAGCCTCAGC 1168
DB 1214 TTACCCAGAGCTCAAGGCTTTGTTCAACATCAGAGAAATTCATCTGTGTAGAAACCTTATG 1273
QY 1169 AATGTAAAGAGTGTGGAGAGCCCTTTCGCTGGGTTTCAGGCCCTGTAAAGCAGAGAGA 1228
DB 1274 AGTGAAGAGAAATGTGGCAAGGCTTTATGATGAGCTCAGCACTTATCATATCAGAGAA 1333
QY 1229 TACATACGGGCGAGAGAGCCGTACAAAGTGCACAGAAATGTGGAGAGCCCTTCAATTGGCT 1288
DB 1334 TTCACTACTGTGAGAGAAACCTTATGATGTAAAGAAATGTGGAAAGCCTTTTACTCAGAGCT 1393
QY 1289 ATCACTCACTCAGACAGAGAAATCCACACAGAGGAAACCCGATTAATGTAAAGAGT 1348
DB 1394 CACAGCTTGTACATCAGAGAAATTCACGCTGTGAGAAACCTTTGAAATGTCTGAAT 1453
QY 1349 GTGGAGAGCCTTTCATTTATGATCGAGCCTCGTGAACATGAGAAATTCATACCGGGG 1408
DB 1454 GTGGGAGAGCCTTTTACTCAGAACTCAAACTTTTCACAGATCAGAGAAATTCATACAGATG 1513
QY 1409 TGAACCTTATGGGTGTAAGAAATGTGGAGAGCTTTATGTCACGGCCATCAGCTTACAC 1468
DB 1514 AAAAACTATGAATGTATGATGATGTGAAAGGCCCTTAAATGAATGCTCAACCTTACTC 1573
QY 1469 AACATCAAGAAACGACAGGTGGGGGGAATCTCTAGAAATGTAAAGAGTGGGGAGAGGAT 1528
DB 1574 GACATCTGAAATTTACCTGCTGTAAGAGCCCTTATACCTGTAAAGAAATGTGGAAAGCCTT 1633
QY 1529 GTAACCACTTAAACCATCTCCAGAAATCATCAGAGAGATCCACACAGT 1575
DB 1634 TTAGTAGTGGCTCGGATCTCATTCGTCAACAGGAAATTCATATCTAT 1680

RESULT 8
US-09-620-312D-163
; Sequence 163, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drenth, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 163

```

LENGTH: 2925
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (178) .. (2433)
US-09-620-312D-163

Query Match 23.7%; Score 478.2; DB 3; Length 2925;
Best Local Similarity 66.9%; Pred. No. 5.3e-141;
Matches 677; Conservative 0; Mismatches 335; Indels 0; Gaps 0;

559 CATCATAGAGAGATTCCTTTGATGTAAGAGCTGTGGAGAGCCCTTAGTGTGCTAT 618
1159 CATACTGGGAGAGACCATACCTTTAATGATGTGAAAAGCCTTTAGCCAGAGAGC 1218
619 CAACCTTATGCAACATGAAAAATCCCTACTGTGTGAAAACCTTATGAAATGAATGT 678
1219 CACTTATGTGAACATCAGAAAATTCATACGGGAGAAAACCTTTAAATGTGATGT 1278
679 AAGAGAGCCCTCCGTTGGGCAATCAGCTTACATCAATCAAAAATTCATCTGGGAG 738
1279 GATTAACCTTACCCAGAGACACACTTACTCAATCAAAAATTCATCTGGAGAA 1338
739 AAGCCTACGAATGTAAGAATGTGTGAAAGCTTTTCATGGGCTCAAGCCTGTTATT 798
1339 AAAACCTATTAATGTATGAAATGTGAAAAGCCTTCAAGGGCCCTCACTTTATCCGT 1398
799 CATTAAGAGATTCATCTGTGAAAAACCTATGAAATGTAAGAATCTGTGAAAAGCCTTT 858
1399 CATCATATATTCATCTGTGTGAAAAACCTATGAAATGTAAGAATGTGTGAAAAGCCTTT 1458
859 CGGCGTGTGATGAGCTCACTAGACACAGAGATTCACACTGSGGAGAAAAGCTACGAA 918
1459 AGCCAGACTCAAACTCTCACTAGCATCAAAAATCTATCTGGAGAAAACCTTATGAT 1518
919 TGCAAAAGACTGTGTGGAAGACCTTTAGCCGTGTATTAACCTTATGAGCAAGAGAAAT 978
1519 TGTGCAATGTGTGAATAATCTTTAGTTACTGTCTATCCCTTCAAGCCTGAATAAT 1578
979 CATAGTGGGAGAGAGCCTTACAGTGTAAAGACTGTGGAGAGCCTTTATTTGTGTTCA 1038
1579 CATACTGGAGAAAACCTTACAAATCAATGATGTGAAAAGCCTTCACTCTCA 1638
1039 AGCCTCATTCAGAGATAAAGAAATTCACAGTGTGAAAACCTATGAAATGTCAAGATGT 1098
1639 TCCCTTACTCAATCGGAGAAATTCACAGAGAAAAGCCTTTGATGTGATGTGT 1698
1099 GGGAGAGCCTTTATCTGAGTCAATTAACCTTACAGCATCAAGAGATCCACCGGTGAG 1158
1699 GGAAGAGCTTTCAAGTTATCTCTCAAACTTATCAGATCAGAAAATCTCATCTCAAGAG 1758
1159 AAGCCTCAAGAAATGTAAGAGTGTGGAGAGCCTTTGCTGTGGGTTCGAGCCTGTTAAG 1218
1759 AAGCTTATGAATGTAAGAAATGTGGAAAAGCTTTTATTCGAGTTTCTTTGCTAAG 1818
1219 CACGAGAGATACATACGGGCGAAGAGCGTACAGTGCACAGAAATGTGGAGAGCCTTT 1278
1819 CATGAAGAATTCATCTGTGAGAAAACCTTATCAGTGTATGAAATGTGGAGAAAACCTTT 1878
1279 AATTGTGCTATCACTCACTCAGCAGAGAGATCCACAGCGAAAACCCGCTATAAA 1338
1879 AGTTATGTTCATCCCTTATTCAGCATAGGAAGTCCATCTGGAAGAACCTTTCAAG 1938
1339 TGTAAAGATGTGTGGAAGGCTTTTATTTATGATTCGAGCTCGTGAACATGAGAAAT 1398
1939 TGTAAAGATGTGTGGAAGATTCACAGAACATACACCTTACACGCTAAAGAGAAAT 1998
1399 CATACGGGAGTGAACCCCTATGGGTGTACAGAAATGTGGAGAAAGCTTTTACTGACGGCAT 1458
1999 CATACGGAGCCAGCCTTATGTGTGTCTGAGTGTGTGTAAGCCTTTGACACTTTGTTC 2058
1459 CAGCTTACACAAATCATGAAAACGCAAGTGGGGCGAAATCTTAAGAAATGTAAGAGTGC 1518

2059 TCTCTTGCTCAACATCAAAAACTCACAGAAAGAAAACCTACAGGTATTAATGT 2118
1519 GGGAGGAGATGTAAACCATTAACCTCTCGAGAAATCAGAGATCCACA 1570
2119 GAAAAGACCTTTAGCGAGAGCTCCATCTTAACCTACGATCAAGAAATTCACA 2170

RESULT 9

US-10-104-047-693
Sequence 693, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cdna
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
PRIOR FILING DATE:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 693
LENGTH: 2241
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-693

Query Match 23.6%; Score 474.8; DB 3; Length 2241;
Best Local Similarity 65.9%; Pred. No. 5.4e-140;
Matches 705; Conservative 0; Mismatches 362; Indels 3; Gaps 1;

422 TTGGCCGTAACTGATATGTGAAGTACGCTTGAAGAACACAGAGCGCTCAGAGGAGGT 481
1169 TTGGAGATGTTTGAATATAGAGCACTTGCAAAAACAATGGATATCCAAATGGGC 1228
482 ATGTCAATGATGATCATCAATTAATGCAAAAAGCCTGTCTATAGAGAGGACCCCTC 541
1229 ATTTATGTAAGAAATATTCACCTCGAATATACGCCCATTTATTCACAGACATTC 1288
542 CTAGAACATATCAGAGA---CATCTAAGAGAAATTCCTTGAATGTAAGAGCTGTGGGA 598
1289 TTAATCTCATCAATTAATTAATTAATGAAGACAGACCTATGAATGAATGTGAA 1348
599 AGGCTTTAGTGTGCTTCACTTCACTTCACTCAATCAGAAAATCCATCTGTGTGAGAAAC 658
1349 AGGCTTTAGTGTGCTTCACTTCACTTCACTCAATCAGAAAATCCATCTGTGTGAGAAAT 1408
659 CTATGATGTAAGAAATGTAAGAGGCTTCCGTTGGGCAATCAGCTTACTCAATC 718
1409 CTATGAAATGTAAGAGTGTGGAAAATCTTTAGTTGTGTTCACATGTTACTCGGCATC 1468
719 AAAAAATCATCTGCGGAGAGAGCCCTTACGAATGTAAGAATGTGGAGAGCCTTTTCAT 778
1469 TGAATAATCATCTGCGGAGAGAGCCCTTGAATGTAAGAAATGTGGAGAGCCTTTGAGTT 1528
779 GGGGCTCAAGCCTCGTTATTCATAGAGGATTCATCTGTGTGAAAACCTTATGAATGTA 838
1529 GTAGCTCATACCTTTTCAACATCAGAGAAATCATACCGGTAAAGAAACCTTATGAATGTA 1588
839 AAGACTGTGAAAAGCCTTTGCGGTGTGATGAGTCACTCAGACCAAGAAATTCACA 898
1589 AGGAATGTGGAGAGGCTTTAGTTATTTGCTCAAAATCTTATGACCATACGCAATTCACA 1648
899 CTGGGAGAAAAGACTACGAATGCAAGAGCTGTGGAGAGCCTTTAGCCGTGTATTAAC 958
1649 CTGGTAAAAACCTTATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1708
959 TTAATGAGCAAGAGAAATTCATAGTGTGGGAGAGCCTTACAGATGTAAGAGCTGTGGGA 1018
1709 TTTTTCAGATGACGAATTCATACAGGTGAGAGAAACCTTATGATGTAAGAAATGTGGCA 1768
1019 AGGCTTTATTTGTGTTCAGGCTCATTCAGCATTAAGAAATTCACAGAGGTGAGAAAC 1078

Db	1769	AAGCTTTATCCCAAGCTCAAAGCTTGTCTTCAACTCAGAGAAATTCATCTGTGTAGAAAC	1828
Qy	1079	CTATGAAATGCAAGAAATGTGGAAAGCCTTTACTCGAGTCAAATTAACCTTACTCAGATC	1138
Db	1829	CTATAGTGTGAAGAAATGTGGCAAAAGCCTTTAGTAGTGCTCAGCACTTACTATATC	1888
Qy	1139	AGAAGATCCACACCGGTGAGAAAGCTTCACGATGTAAAGAGTGTGGGAAGCCTTTGCT	1198
Db	1889	AGAGAAATTCACACTGTGTAGAAACCTTATGATTTGTAAAGAAATGTGGAAAGCCTTTTACTC	1948
Qy	1199	GGGTTTGAGAGCTCGTTAAGACAGAGAAATCACTACGGGGGAAAGCCGTCACAAATGCCA	1258
Db	1949	AGAGCTACAGACTTCGTCAACATCAGAGAAATTCACGCTGTGAAAGAACCTTTGAAATGTC	2008
Qy	1259	CAGAAATGTGGAAAGCCTTCAATTTGTGGCTATCACTCACTCAGACAAGAGAAATTCACA	1318
Db	2009	TTGAAATGTGGAAAGCCTTTACTCAGAACTCACAACCTTTTCAGACTCAGAGAAATTCATA	2068
Qy	1319	CAGCGGAAACCCCGTATTAATGTAAAGAGTGTGGAAAGCCTTTCATTTATGATCGAGCC	1378
Db	2069	CAGATGAAAAACCATATGAATGTATGAATGTGAAAAGCCTTTTATTAATATGCTCAAAAC	2128
Qy	1379	TTCGTAACCATGAGAGAAATTCATACCGGGGTGAAACCTTATGGGTGTACAGAAATGTGGGA	1438
Db	2129	TTACTCGACATCTGAGAAATTCACACTGTGTAAAAAGCCTTATATACGTATAAGAAATGTGGGA	2188
Qy	1439	AGAGCTTTAGTCAGAGCGCATCAGCTTACACAACATCGAAGAAACGACAGT	1488
Db	2189	AGGCTTTTAGTAGTGCTCGGATCTCAATTCGTCACTCAGGAAATTCATACT	2238

Db	1033	CTGGGGGAAAACCTTATGCTATGTAAGATTGTGGAAAGCCTTCAAGTCAGAAATCCAAATC	10922
Oy	875	TCACCTAGCACACAGAGATTCACACTG3GGGAGAAAGACTAGAAATGCAAAAGCTGTGGGA	934
Db	1093	TCAATTGAACATGAGCGAATTCACACTGGAAGAAACCCTATGATGTGTAAGAAATGTGGGA	11522
Oy	935	AGACCTTTAGCCGTGTGTATTAACCTTATTCAGCAACAAGAGATTCATATGTGGGAGAAAC	994
Db	1153	AATCCCTCAGCGAACAACCAAAATCTTTATGTGAGCAGAGAAAATTCATATCTGGGAGAAAC	12122
Oy	995	CTTACAGATGTAAGAATGTGTGGGAAAGCCTTTATTTGTGTCTAAGCTCAATTACAGATA	10542
Db	1213	CTTATGATGATTAAGTAATGTGTGAGACCTTTTCTCGAATGTCAATCTGTTCACCTACATA	12722
Oy	1055	AAAGATTTCCACACAGGTGAGAAACCCATGTAATGTCAAGAATGTGGGAAAGCCTTTACTC	11142
Db	1273	TGAAAGTCCACACAGGGGAGAAACCCCTATTAATTAATTAATGTGAGAAAGCCTTTCTCTC	13322
Oy	1115	GAGTCAATTACCTTACTCAGCATCAGAAAGATTCACACCGGTGAGAAAGCCTTCACGAATGTA	11742
Db	1333	AATCCTCAGATTTTATTTATATACATATGGAAGTCAACACTGGGTGAGAAACCCATGTATGTA	13922
Oy	1175	AGGAGTGTGGAGAGGCTTTTGTGCTGGGGTTTCGAGCCTCGTTAACACGAGAGATACATA	12342
Db	1393	GTGATGTGGGAAAGCCTTCTCTCAGAGTTCAATCCCTAACCGTACATATGGAATACATA	14522
Oy	1235	CGGGCGAGAAAGCCCTACAGTGCACAAGATGTGGAAAGCCTTCAATTGTGTATCAACC	12942
Db	1453	CAGCTTGAGAAACCTTATGAATGTAGAAATGTGGAAAGCCTTACAGACAGAAAGAAATTC	15122

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RESULT 10
US-10-104-047-1464
; Sequence 1464, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1464
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-104-047-1464

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Db	1513	TCATTACACATCAGAAAAATTCACACCTGAGAGAAACCTTATGATTCAGATGTAATGTGGGA	15722
Qy	1355	AGGCTTTCAATTATGATTCGAGCCTGCTGAAACATGAGAGAAATTCATATCCGGGGTGAAC	1414
Db	1573	AAGCTTTATTCAGATGTCAAACCTCATTCGACACCGAGAGAAATTCATACGGGTGAGAAAC	16322
Qy	1415	CCATATGGGTGACAGATATGTGGGAAGACCTTATGTCAGGCGATCAGCTTACATCAATATC	1474
Db	1633	CCATATGATGTACAGTATGTGAAAAACCTTTATGTCGAAATCAAACCTTCATGAAACATG	16922
Qy	1475	AGAAATGCGCAGATGTGGGGCGAAATCTTCAGCATGTGAAGAAGTGGCGGAAGCATGTAAAC	1534
Db	1693	AGAAATTCATCTACTGAGAGAAACCTTATCATTTGATTCATATGTGGGAAAGCTTTCAGTC	1752
Qy	1535	ACCTTAACCATCTTCGAGGAACATCAGAGATCCACA	1570
Db	1753	AGAGACAAAATCTCTTGAGAGATGAAAAAAATTCATA	1788

	Query Match	22.9%	Score 461.6;	DB 3;	Length 1914;
	Best Local Similarity	66.5%	Pred. No. 7,8e-136;		
	Matches 662;	Conservative 0;	Mismatches 334;	Indels 0;	Gaps 0;
Qy	575	CCTTTGATGTAAAGACTGTGGGAAGCCCTTTAGTCGTGCTATCAACATTGACAATC	634		
Db	793	CCTTTAA GTTAATCACTGTGACAMAACTTCACTCAATAATTTGACCCTCATTTAGACATG	852		
Qy	635	AGAAAAATCCATPACGTGTGAGAAACCTTAGTAATGAATGAATGAAGAAGGCCCTTCGCTT	694		
Db	853	AGCGAATTCATGCTGAGAGAAACCTTAGCATTTAAAGATGTGAAAAGCCTTCACGTA	912		
Qy	695	GGGGCAATCAGCTTACTCAAATCAAAAATTTACTGTGGGAGAGCCCTCACGATGTA	754		
Db	913	GGAAAGAAAAATCTTATTAACATCAGAAAATTTCACTACGTGGGAAAAAACCGATTAAGTGA	972		
Qy	755	AAGACTGTGGAGAGGCTTTTCGATGGGGGCTCAACCTCGTATTCAATGAAGATGCATATA	814		
Db	973	ATGATATGTGAAAAGCTTTCAATTAGATGTCAAACTTATTATTAAGCACACAGAAATTCATA	1032		
Qy	815	CTGGTGAAAAACCCCTATGAATGTAAAGACTGTGAAAAGGCCCTTTCGGCGTGATGATGAC	874		

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RESULT 11
US-09-949-016-4204
; Sequence 4204, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERE
; FILE REFERENCE: C001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4204
; LENGTH: 3798

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TYPE: DNA
ORGANISM: Human
US-09-949-016-4204

Query Match 22.9%; Score 460.6; DB 3; Length 3798;
Best Local Similarity 64.9%; Pred. No. 2.5e-135;
Matches 682; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

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QY 535 ACCCTCTAGAAACATGAGAGACATCATTAAGAAATTCCTTTGAAATGTAAGACTGT 594
DB 1816 ACCCTTAATAGACATTAAGAGAGACACACTGAGAGAAACCTTCAAAATGTGAAGATGT 1875
QY 595 GGGAGGCGCTTTAGTGTGCTATCACTTAAGTCAATCAAGAAATTCATCTGTGTAG 654
DB 1876 GCGAAAGCTTTTAGCATTTCTTCAACCTTGTCAAAATGAAGAAATTCATCTGAGAG 1935
QY 655 AAACCTTAAGATGTAAGAAATGTAAGAGGCTTCCTGTTGGGCAATCAGTCTACTCA 714
DB 1936 AAACCTTAAGATGTAAGAAATGTAAGAGGCTTTTAAAGCTTTCACCTTGTCTAA 1995
QY 715 CATCAAAAAATTCATCTGAGGAGAAAGCCCTAAGAAATGTAAGAGTGTGGAAGCTTTT 774
DB 1996 CATTAAGAAATTCATCTGAGAGAAACCTTCAAAATGTAAGAAATGTGCAAGCTTTT 2055
QY 775 CGATGGGCTCAAGCTCTTATTCATTAAGAGATTCATCTGTGAAAAACCTTATGAA 834
DB 2056 AGCAATTTCTCAACCTTGTCTATCATTAAGATTCATCTGAGAGAAACCTTACAAA 2115
QY 835 TGTAAAGATCTGTGGAAGGCTTTTGGCGTGTGATGAGTCACTAGCAACGAGATTC 894
DB 2116 TGTAAAGATGTACAAAACTTTTAAAGCACTCTCAACCTTCAAACTTAAATTA 2175
QY 895 CACACTGGGAGAAAGCTACGATGCAAAAGCTGTGGAAGACCTTTAGCGTGTAT 954
DB 2176 CATGCTGGAGAGAACTCTTAAGATGTAAGAAATGTGCAAGCTTTTATCATCTCA 2235
QY 955 AAACCTTATTCAGACAAGAAATTCATAGTGGGAGAGGCTTTACGATGTAAGACTGT 1014
DB 2236 AATCTTAATATCATTAAGTTTATTCATTAAGAGAAACCTTCAAAAGTGAAGATGT 2295
QY 1015 GGGAGGCTTTTATTTGTGTGCTCAAGCTCATTCAGATTAAGAAATTCACAGGTGAG 1074
DB 2296 GGGAAAGCATTTTAACTGTGCTCAAGCTTCAAAATTAAGAAATTCATCTAGAGAG 2355
QY 1075 AAACCTTATGATGTCAAGATGTGGGAAGGCTTTTACGATGCAATTCCTTACTCAG 1134
DB 2356 AAACCTTCAAAATGTAAGAAATGTGGAAGCAATTTATGTGCTTCAACCTTAAGTGA 2415
QY 1135 CATCAGAAATTCACACCGGTGAGAGGCTTCAAGATGTAAGAGTGTGGAAGGCTTTT 1194
DB 2416 CATTAAGAGATTCACACTGAGAGAGGCTTCAAAATGTAAGAAATGTGCAAAAGCTTTT 2475
QY 1195 CGGTGGGCTTCAAGCTCTGTTAAGCAAGAGATTCATAGCGGCGAGAGGCTTCAAG 1254
DB 2476 AGCGTTTCTCAACCTTACTTAAGCATTAAGCAATTCATCTGAGAGAAACCTTACAAA 2535
QY 1255 TGCAAGAATGTGGAAGGCTTCAATTTGTGCTATCACTCACTGAGCAAGAGATC 1314
DB 2536 TGTAAAGAAATGTGGAAGGCTTTTAAAGCACTCTCAGCGCTTGTAAACATTAATA 2595
QY 1315 CACACAGGCGAAACCCGTATTAATGTAAGAGTGTGGAAGGCTTTCAATTTATGATCG 1374
DB 2596 CATGCTGAGAGAAACCTTCAAAATGTGAGAAATGTGCAAAAGCTTTTAAATCATCTTCA 2655
QY 1375 AGCTGTGTAAGATGAGAAATTCATACCGGGGTGAACCTTATGAGTGTACGAATGT 1434
DB 2656 AATCTTAAGCAATTAAGATTAATTCATTAAGAGAAACCTTCAAGAGTGAAGATGT 2715
QY 1435 GGGAGAGCTTTAGTCAAGGCTCATGCTTACACAAATCATCAAGAAACGCAAGTGGGCG 1494
DB 2716 GAGAAAGCAATTTATGTGTCTCAACCTTACTGAACATTAAGAAATTCATCAAGAGAG 2775
QY 1495 AAATCTTAAGATGTAAGAGTGTGGAAGGCAATGTAACCACTTAAACATCTCCGAGAA 1554

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DB 2776 AAACCTTAAGATGTAAGAAATGTGCAAAAGATTTAGCACTTACACCTTACTACA 2835
QY 1555 CATCAGAGATCCACAAAGCTTGAAGGCT 1585
DB 2836 CATTAAGAGATTCACACTGAGAGAAACCTT 2866

```

RESULT 12

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US-09-949-016-12227
; Sequence 12227, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12227
; LENGTH: 156942
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(156942)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12227

```

Query Match 22.9%; Score 460.6; DB 3; Length 156942;
Best Local Similarity 64.9%; Pred. No. 2.7e-134;
Matches 682; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

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QY 535 ACCCTCTAGAAACATGAGAGACATCATTAAGAAATTCCTTTGAAATGTAAGACTGT 594
DB 152967 ACCCTTAATAGACATTAAGAGAGACACACTGAGAGAAACCTTCAAAATGTGAAGATGT 153026
QY 595 GGGAGGCGCTTTAGTGTGCTATCACTTAAGTCAATCAAGAAATTCATCTGTGTAG 654
DB 153027 GGGAAAGCATTTTAACTGTGCTCAAGCTTCAAAATTAAGAAATTCATCTAGAGAG 153086
QY 655 AAACCTTATGATGTCAAGATGTGGGAAGGCTTTTACGATGTAAGACTGT 714
DB 153087 AAACCTTAAGATGTAAGAAATGTGCAAAAGCTTTTAAAGCTTTCACACCTTGTCTAAA 153146
QY 715 CATCAAAAAATTCATCTGAGGAGAGGCTTCAAGATGTAAGAGTGTGGAAGGCTTTT 774
DB 153147 CATTAAGAAATTCATCTGAGAGAAACCTTCAAAATGTAAGAAATGTGCAAAAGCTTTT 153206
QY 775 CGATGGGCTCAAGCTCTGTTTATTCATTAAGAGATTCATCTGTGTAAGAAACCTTATGAA 834
DB 153207 AGCAATTTCTCAACCTTGTCTATCATTAAGATTCATCTGAAGAAACCTTACAAA 153266
QY 835 TGTAAAGATGTGGAAGGCTTTTGGCGTGTGATGAGTCACTGAGCAACGAGATTC 894
DB 153267 TGTAAAGATGTGCAAAACCTTTTAAAGCACTCTCAACCTTCAAAATTAATA 153326
QY 895 CACACTGGGAGAAAGCTTCAAGATGCAAAAGATGTGGAAGGCTTTAGCGTGTAT 954
DB 153327 CATGCTGAGAGAAACCTTCAAAATGTGAAGATGTGCAAAAGCTTTTAAATCATCTTCA 153386
QY 955 AAACCTTATTCAGACAAGAAATTCATAGTGGGAGAAAGCTTACGATGTAAGACTGT 1014
DB 153387 AATCTTAATATCATTAAGTTTATTCATCTGAGAGAAACCTTCAAAAGTGTGAAGATGT 153446

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RESULT 13
US-09-949-016-15946
; Sequence 15946, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15946
; LENGTH: 156950
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) _(156950)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15946

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QY	535	ACCCTTCCTGAACACATCTAGAGACATCATPAGAGAAATTCCTTGAATGTAAGACGTG	594
Db	152967	ACCTTAACCTGAACATPAGAGATACACTGAGAGAAACCTTCAAAATGTGAAGAAATGT	1530
QY	595	GGGAGAGCCTTTTGTGCTGGCTATCAACTTAAGTCAACATCAGAAATCACTACTGTGAG	654
Db	153027	GGCAAACTTTTGTGCGATTCCTTCAACCTTGTCTAAAATPAGAGAAATTCATCTAGAGAG	1530
QY	655	AAACCTTATGAATGTAAAGATGTAGAAGCCTTCCTGTGGGCAATCAGCTTACTCA	714
Db	153087	AAACCTTACAAATGTGAAGATGTGGCAAAAGCTTTTACCGTTCCTTCAACCTTGTCAAA	1531
QY	715	CATCAAAAAATTCATACTGGGGGAAGCCCTACGAATGTAAAGCTGTGGGAAGGCTTTT	774
Db	153147	CATPAGAAATTCATCTAGAGAGAAACCTTCAAAATGTAAAGATGTGGCAAGCTTTT	1532
QY	775	CGATGGGGCTCAAGCCTCGTTATTCATPAGAGATTCATCTGTGTGAAAAAACCTTATGA	834
Db	153207	AGCAATTCCTCAACCTTGTCTAATCATPAGATTAATCATCTGAAGAGAAACCTTACAAA	1532
QY	835	TGTAAAGACTGTGGAAGAGCCTTTCCGCGTGTGATGAGCTCACTCAGCACAGAGATTC	894
Db	153267	TGTAAAAATGTGCACAAACCTTTTAAACGACTTCAACCTTTATPAAACATPAAATATATA	1533
QY	895	CACACTGGGAGAAAGCTACGATGCAAGAAAGCTGTGGGAGAAAGCCTTTAGCCGTGTGAT	954
Db	153327	CATGCTGAAGAGAACTCTCAAAATGTGAAGATGTGGCAAGCTTTTATCGATCTTCA	1533
QY	955	AAACTTATTCAGCAACAAGAAATTCATAGTGTGGAGAGCCTTACGATGTAAAGACTGT	1014
Db	153387	AATCTTACTPACATAAGTTTATTCATACGTGAGAGAAACCTTCAAGTGTGAAGAAATGT	1534
QY	1015	GGGAAGCCTTTTATTTGTGCTCAAGCCTCAATTCAGATATAAGATTCACACAGGTGAG	1074
Db	153447	GGCAAAACATTTTAACTGTGCTCTCAAGCTTACATAAATPAAAAATTCATACTAGAGAG	1535
QY	1075	AAACCCATGATGAATGTCAAGATGTGGGAGAGCCTTTACTCGAGTCAATTCCTTACTCAG	1134
Db	153507	AAACCTTCAAAATGTAAAGATGTGGCAAAAGCATTTTATGTGCTTCAACCTTAACTTGA	1535
QY	1135	CATCAGAAAGATCCACACCGGTGAGAAAGCCTTACGAATGTAAAGAGTGTGGAGAGCCTTT	1194
Db	153567	CATPAGAGATTAACACTGAGAGAGAAACCTTACAAATGTGAAGATGTGGCAAGCCTTTT	1536
QY	1195	CGCTGGGGTTCGAGCCTCGTTAAGCAAGAGAGATATATCCGGCCGAGAGCCCTTACAAG	1254
Db	153627	AGCGGTTCCTCAACCTTCTAAGCAATMAACAATTCATCTGTGAGAGAAACCTTACAAA	1536
QY	1255	TGCACAAATGTGGGAAGAGCCTTCAATGTGTGCTATCACTCACTCAGCAAGAGAGATC	1314
Db	153687	TGTAAAGAAATGTGGCAAGCCTTTTAAACCACTCTCAGCCCTTGTGTAAACATPAAATATA	1537
QY	1315	CACACAGGCGAAACCCCGTATPAAATGTAAAGAGTGTGGAGAGGCTTTCATTTATGATCG	1374
Db	153747	CATGCTGAAGAGAAACTCTCAAAATGTGAAGAAATGTGGCAAGCCTTTTAACTCATCTTCA	1538
QY	1375	AGCTCTGTGAACATGAGAGAAATTCATACCGGGTGAACCCCTATGTGTGTAACGAATGT	1434
Db	153807	AATTTTACGACACATPAGATTAATTCATPAAAGAGAAACCTTTCAAAGAGTGAAGAAATGT	1538
QY	1435	GGGAAGAGCTTTTGTGTCAGGCACTCAGCCTTACACAACTCAGAGAAACGCAACAGTGGGCG	1494
Db	153867	GACAAACACATTTATCTGTGTCTCAACCTTCTAGTAATPAGAGAAATTCATACAGAGAG	1539
QY	1495	AAATCTTACGAATGTAAAGAGTGTGGGAGAGGCAATGTAAACCACTTAAACATCTCCAGAA	1554
Db	153927	AAAACTTACAAATGTGAAGATGTGGCAAAAGCATTTTGTGACAGCCTTCAACCTTACTACA	1559
QY	1555	CATCAGAGATCCACAACAGTTGAAGAGCCT	1585
Db	153987	CATPAGAGATGCACACTGAGAGAAACCTT	154017

RESULT 14
 US-10-104-047-271
 ; Sequence 271, Application US/10104047
 ; Patent No. 6943241
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. 6943241el full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 271
 ; LENGTH: 2669
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-104-047-271

Query Match 22.7%; Score 456.6; DB 3; Length 2669;
 Best Local Similarity 65.4%; Pred. No. 3.8e-134;
 Matches 669; Conservative 0; Mismatches 354; Indels 0; Gaps 0;

QY 568 GAGAAATTCCTTGAATGTAAAGACTGTGGGAGGCGCTTATGTCGCTATCACTTAGT 627
 DB 1159 GAGAAACCTTACGAGTGTATGACTGTGGGAAAGCGTTCAATGTATGCAAAATTAATT 1218
 QY 628 CAACATCAGAAATTCATCTACTGTGTGAGAAACCTTATGAATGTAAAGATTAAGAGGCC 667
 DB 1219 CAACATCAGAAATTCATCTACTGTGTGAGAAACCTTATGAATGTAAAGATTAAGAGGCC 1278
 QY 688 TTTCCGTTGGGGCATCAGCTTACTCAACATCAAAATTCATCTGCGGAGAGCCCTTAC 747
 DB 1279 TTCAAGTGCAGCTCCAGCTTACGAGCATCAAGCATCCACAGAGAAAGCCCTAT 1338
 QY 748 GAATGTAAAGACTGTGGGAAAGCGCTTTCGATGGGCTCAAGCCTGTTATTCATTAAGAG 807
 DB 1339 CAGTGTAAAGAGTGTGAAAGAGCGCTTCAATTAATTAATCAAAATTCATTCAGCATCAGAG 1398
 QY 808 ATTCAATCTGTGTGAAAGAGCGCTTATGAATGTAAAGACTGTGGAAAGCGCTTCCGCTGT 867
 DB 1399 ATCCACACAGTGTGAAAGAGCGCTTATGAATGTCACTGAATGTGAAAGAGCGCTTCACTGT 1458
 QY 868 GATGAGCTCACTGAGACCGAGATTCACACTGGGGAGAAAGCTACGAATGCAAGAG 927
 DB 1459 GGGAACTTAATCCAAACCGAGATTCACACAGGCGAGAAAGCCCTATGAGTGAATGA 1518
 QY 928 TGTGGAGAGACTTTAGCCGTGTGTATTAATTATCAGCAAGAGAAATTCATAGTGG 987
 DB 1519 TGGGGAGAGCGCTTCAGATGTAACTCCCAATTCGGAGAGATCTGAGAAATTCACACTGG 1578
 QY 988 GAGAGCGCTTACAGTGTAAAGACTGTGGAGAGCGCTTTATTTGTGTTCAAGCTCAT 1047
 DB 1579 GAGAAAGCGCTTATGAGTGTAAAGAGCGCTTTCAGCGTTATGAGAAAGCTTAATG 1638
 QY 1048 CAGCATTAAGATTAATCAACAGGTGAGAAAGCGCTTATGAATGTCAAGATGTGGAGAG 1107
 DB 1639 CGGATCAGAGATTCACACTGGGAGAAAGCGCTTTGAATGTATGAGTGTGGAGATGC 1698
 QY 1108 TTTACTCGAGTCAATTAATCTTACTCAGCATCAGAAAGATTCACACCGGTGAGAGCGCTCAC 1167
 DB 1699 TTTACTTCTAAAGAAAGCTTACTGATCATCAAGATTCATCTGAGAAAGAGCGCTTAT 1758
 QY 1168 GAATGTAAAGAGTGTGGAGAGCGCTTTCGCTGGGCTTCGAGCTCGTTAAGCAGAGAG 1227
 DB 1759 CATGTAAAGAAAGTGTGGAGAGCGCTTTCAGTATCAATGCCAAATCTAATGAGCATCAGAG 1818
 QY 1228 ATACATACGGGCGAGAGCGCTACAGTGCAGAAATGTGGAGAGCGCTTCAATTTGGGC 1287
 DB 1819 ATTCAATCTGGGAGAGAGCGCTTTCATTAATGTATGAGAAATGTGAGAAAGCATTCAGCTGTAGT 1878

QY 1288 TATCACTCTCACTCAGACAGAGAAATTCACACAGCGGAAAGCCCGTATTAATGTAAAGAG 1347
 DB 1879 TCTAATCTAATATTGTCCACAGAGAAATTCATACAGAGAGAAAGCCCTTCAGTGTAAAGAG 1938
 QY 1348 TGTGGAGAGCGCTTCAATTAATGTGATCGAGCGCTCGTGAACATGAGAGATTCATACCGGG 1407
 DB 1939 TGTGAGAAAGCGCTTCAGTGTATGCGCATTTAATTTGCGCATCAGAGAGCCACACTGGG 1998
 QY 1408 GTGAAAGCGCTTATGGGTGTACAGAAATGTGGAGAGCGCTTATGTCAGGCGCATGAGCTTAC 1467
 DB 1999 GAGAAAGCGCTTCAAGTGTGTGAAATGTGGCAAGGCTTCAGCTTATGTTCTGATCATTT 2058
 QY 1468 CAACATCAGAAAGCGACAGTGGGCGGAAATCTTACGAATGTAAAGAGTGTGGAGAGCG 1527
 DB 2059 ATACACAGACAGTCCACACTGTGAAAGAAAGCGCTTATGTGTGTGTGTGGAGAGCA 2118
 QY 1528 TGTAAACCACTTAACCATTCGGAAGCATCAGAGATTCACAAAGCTTGAAGAGCGCTTT 1587
 DB 2119 TTCAAGTGTAGCTTCCAGCTCAGTCAAGATGTCCATTAATGTGAGAGAAATCTTAA 2178
 QY 1588 TGA 1590
 DB 2179 TAA 2181

RESULT 15
 US-09-949-016-485
 ; Sequence 485, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 485
 ; LENGTH: 3839
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-485

Query Match 22.6%; Score 455.2; DB 3; Length 3839;
 Best Local Similarity 65.0%; Pred. No. 1.3e-133;
 Matches 673; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

QY 535 ACCCTCTTGAACACATCAGAGCATCATTAAGAGAAATTCCTTGAATGTAAAGACTGT 594
 DB 1688 ACCCTTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1747
 QY 595 GGGAGAGCGCTTATAGTGTGCTATCAACTTAAGCAATCAGAAATTCATCTAGTGGAG 654
 DB 1748 GGGAGAGCGCTTATAGCAATTCACCTTACTACATTAATTAATTAATTAATTAATTAAT 1807
 QY 655 AAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 714
 DB 1808 AAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1867
 QY 715 CATCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 774
 DB 1868 CATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1927
 QY 775 CGATGGGCGCTCAAGCGCTGTTATTCATTAAGAGATTCATCTGAGTGAAGAAAGCGCTTGA 834
 DB 1928 CTATGTCCTCAAGCGCTTAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1987

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 6, 2006, 16:01:11 ; Search time 1223 Seconds
(without alignments)
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Title: US-10-111-257-3
Perfect score: 2015
Sequence: 1 cgcttcgcacacggtgaagc.....gtgaagttcctaactaa 2015

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2015	100.0	2015	5	AAf88159 Human thy
2	1986.8	98.6	2098	4	AA503044 Human dia
3	1967.4	97.6	2173	5	ABa82974 Human tra
4	1958	97.2	2169	4	AAK94562 Human ful
5	1958	97.2	2169	12	ADL31436 Full leng
6	1946.2	96.6	3293	4	AA625944 Human CDN
7	1946.2	96.6	3293	8	ABX73285 Human nov
8	1768	87.7	2010	6	ABN59917 Novel hum
9	1420.2	70.5	1453	4	AAH99589 Human pro
10	1397.8	69.4	1429	11	AD131363 Human CDN
11	1397.8	69.4	1429	13	AD883430 Human lym
12	734.6	36.5	4483	10	ADP14367 Human end
13	703	34.9	2143	8	ABa92946 Human car
14	703	34.9	2143	8	ACA62107 CDNA enco
15	620.6	30.8	2832	10	ADC30401 Human nov
16	620.6	30.8	3547	6	ABn84143 Human zin
17	618	30.7	1945	10	ADA53552 Human cod
18	615.4	30.5	2235	11	ADM03674 Human CDN
19	603.6	30.0	1900	5	AA689495 DNA enco

20	602	29.9	2617	4	AAK53340 Human pol
21	600.4	29.8	2650	4	AAK52356 Human pol
22	593.6	29.5	774	8	AA526388 Human CDN
23	593.6	29.5	774	8	ABX73129 Human nov
24	584.4	29.0	592	12	ACH79967 Human gen
25	575.6	28.6	1521	10	AA155798 CDNA enco
26	573.8	28.5	1749	13	AD068903 Human tum
27	549.8	27.3	2223	4	AB196293 New zinc
28	548.6	27.2	2276	4	AA160063 Human pol
29	546	27.1	1335	12	ADN99068 Human pol
30	546	27.1	1335	12	ADN00637 Novel hum
31	544.4	27.0	1970	13	ADP54658 Human PRO
32	538.6	26.7	1813	5	ABA83028 Human tra
33	538	26.7	2334	10	ADA53517 Human cod
34	538	26.7	4683	5	AA569826 DNA enco
35	520.6	25.8	2274	5	AA158277 Human pol
36	520.6	25.8	2274	5	ADQ98484 DNA enco
37	520.6	25.8	2274	5	ADB48244 Novel hum
38	512	25.4	5718	11	ABE66032 DNA damag
39	510.4	25.3	5718	13	ACN40550 Tumour-as
40	510.2	25.3	526	6	ABL63275 Breast ca
41	510	25.3	1874	8	ABX71104 Novel hum
42	509.2	25.3	1188	8	ABX34452 Human md
43	508.8	25.3	2332	10	ADC30875 Human nov
44	507.6	25.2	3358	9	ACA98941 CDNA enco
45	506.8	25.2	2624	4	AAK94790 Human ful

ALIGNMENTS

RESULT 1	AAf88159	standard; CDNA; 2015 BP.
ID	AAf88159	
XX	AAf88159;	
AC		
XX		
DT	17-JUL-2001	(first entry)
DE		
XX		
XX		
KW	Human thyroid malfunction-associated protein RITA encoding CDNA.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	187..1578
FT		/*tag= a
FT		/product= "RITA"
XX		
PN	WO200127265-A1.	
PD	19-APR-2001.	
XX		
PF	11-OCT-2000; 2000WO-DE003600.	
XX		
PR	12-OCT-1999; 99DE-01049179.	
XX		
PA	(UVBR-) UNIV BREMEN.	
XX		
PI	Bullerdek J, Rippe V, Meiboom M, Belge G;	
XX		
DR	WPI; 2001-290723/30.	
XX		
DR	P-PeDB; AAB86115.	
XX		
PT	New nucleic acid useful for the diagnosis and treatment of thyroid	
FT	disorders, e.g. tumors.	
XX		
PS	Claim 2; Page 52-54; 59pp; German.	
XX		
CC	This invention describes a novel nucleic acid (N1) encoding a polypeptide	
	which comprises a KRAB-domain and/or at least one zinc finger motif. The	

CC products of the invention have cytosolic and antithyroid activity and
CC can be used in gene therapy. Nucleic acids, polypeptides, and antibodies
CC of the invention may be used in the diagnosis and/or the therapy of the
CC malfunction of the thyroid and/or hyperplasias of the thyroid and/or
CC thyroid tumors. They may also be used in the production of medicaments.
CC (N1) can also be used to diagnose thyroid tumors which are located on
CC chromosome 19 at band 19q13. This sequence encodes the thyroid
CC malfunction-associated protein, R19A which is described in the method of
CC the invention
XX

Sequence 2015 BP; 601 A; 444 C; 503 G; 467 T; 0 U; 0 Other;

Query Match 100.0%; Score 2015; DB 5; Length 2015;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTTTGACCGGTGACCAACCGTGTGTCTCCGCCAGTCCGCCAGGCCAGATCCT 60
DB 1 CGCTTCTGACCGGTGACCAACCGTGTGTCTCCGCCAGTCCGCCAGGCCAGATCCT 60
QY 61 TCAGAAAAAGCATCCCGAGAGAGAGAGAGAGATCGTTAAACATCTTAGGCTAGC 120
DB 61 TCAGAAAAAGCATCCCGAGAGAGAGAGAGAGATCGTTAAACATCTTAGGCTAGC 120
QY 121 CTCTCGAAATTTGTCTTCTTCACTGAGTGAACCCCGAGAGAGCTGATCAGTTCT 180
DB 121 CTCTCGAAATTTGTCTTCTTCACTGAGTGAACCCCGAGAGAGCTGATCAGTTCT 180
QY 181 AAAACATATGGCCAGAGGTTTGTGAGCTTCCCGAGAGTACCTTACATTTTTCAGAG 240
DB 181 AAAACATATGGCCAGAGGTTTGTGAGCTTCCCGAGAGTACCTTACATTTTTCAGAG 240
QY 241 GAGTGGCCCTGTCTGAACTCTGCTCAGAGAGAGCCTGTAAGTGGAGAGTGTGAGAG 300
DB 241 GAGTGGCCCTGTCTGAACTCTGCTCAGAGAGAGCCTGTAAGTGGAGAGTGTGAGAG 300
QY 301 TACAGTAACTTGTCTCACTGATTTTGAAGTCAATATGAAAAATGAAGTTTACCTCA 360
DB 301 TACAGTAACTTGTCTCACTGATTTTGAAGTCAATATGAAAAATGAAGTTTACCTCA 360
QY 361 GAAAAAATCATTCATGAATTAAGGCTTCCAAAAGAAATTCAGATGAAGAAATTAATCC 420
DB 361 GAAAAAATCATTCATGAATTAAGGCTTCCAAAAGAAATTCAGATGAAGAAATTAATCC 420
QY 421 CTGGCCGTAATGATGATGTAAGGTAAGCTTGAAGAACACAGAGGCTCAGAGGAGG 480
DB 421 CTGGCCGTAATGATGATGTAAGGTAAGCTTGAAGAACACAGAGGCTCAGAGGAGG 480
QY 481 TATGTCAATCAGATGATCATCAATTAATGCAAAAGGCTGCTAAGAGAGGCAACCTT 540
DB 481 TATGTCAATCAGATGATCATCAATTAATGCAAAAGGCTGCTAAGAGAGGCAACCTT 540
QY 541 CCTAGAACATTCAGAGACATCATTAAGAGAAATTTCTTGAATGTAAGAGCTGTGGAG 600
DB 541 CCTAGAACATTCAGAGACATCATTAAGAGAAATTTCTTGAATGTAAGAGCTGTGGAG 600
QY 601 GCCTTAGTGTGGCTATCAACTTAAGTCAATCAGAAATTCATCTGTGTGAGAACTT 660
DB 601 GCCTTAGTGTGGCTATCAACTTAAGTCAATCAGAAATTCATCTGTGTGAGAACTT 660
QY 661 TATGAATGTAAAGATTAAGAGAGGCTTCCGTTGGGCAATCAGCTTACTCAACATCA 720
DB 661 TATGAATGTAAAGATTAAGAGAGGCTTCCGTTGGGCAATCAGCTTACTCAACATCA 720
QY 721 AAAATTCATCTGTGGAGAGGCTTACGATGTAAGAGCTGTGGAGAGGCTTTTCCATGG 780
DB 721 AAAATTCATCTGTGGAGAGGCTTACGATGTAAGAGCTGTGGAGAGGCTTTTCCATGG 780
QY 781 GGCCTCAGAGCTGTTATTCATTAAGAGATTCATCTGTGAAAAAACCTTATGATGTA 840
DB 781 GGCCTCAGAGCTGTTATTCATTAAGAGATTCATCTGTGAAAAAACCTTATGATGTA 840
QY 841 GACTGTGAAAGGCTTTCCGCGTGTGATGAGCTCACTCAGACCAAGATTCACACT 900

DB 841 GACTGTGAAAGGCTTTCCGCGTGTGATGAGCTCACTCAGACCAAGATTCACACT 900
QY 901 GGGGAGAAAGCTACGAATGCAAGACATGTGGAGAGCTTTAGCCGTGTGTAATACCT 960
DB 901 GGGGAGAAAGCTACGAATGCAAGACATGTGGAGAGCTTTAGCCGTGTGTATTAACCTT 960
QY 961 ATTCAGACAAGAGAAATTCATAGTGGAGAGAGCTTACGAGTCAATTAAGCTGTGGAG 1020
DB 961 ATTCAGACAAGAGAAATTCATAGTGGAGAGAGCTTACGAGTCAATTAAGCTGTGGAG 1020
QY 1021 GCTTTTATTTTGTGTTCAAGCTCATTCAGCTTAAAGAAATTCACACAGGTGAGAAACC 1080
DB 1021 GCTTTTATTTTGTGTTCAAGCTCATTCAGCTTAAAGAAATTCACACAGGTGAGAAACC 1080
QY 1081 TATGAATGTCAAGAAATGTGGAGAGGCTTTACTCGAGTCAATTAAGCTTACGATCAG 1140
DB 1081 TATGAATGTCAAGAAATGTGGAGAGGCTTTACTCGAGTCAATTAAGCTTACGATCAG 1140
QY 1141 AAGATCCACACCGGTGAGAGGCTTACGAAATGTAAGAGGTGTGGAGAGGCTTTGCTGG 1200
DB 1141 AAGATCCACACCGGTGAGAGGCTTACGAAATGTAAGAGGTGTGGAGAGGCTTTGCTGG 1200
QY 1201 GGTTCGAGCTCTGTTAAGCAGAGAGATACATACGGGCGAGAAACCTGTAAGTCCACA 1260
DB 1201 GGTTCGAGCTCTGTTAAGCAGAGAGATACATACGGGCGAGAAACCTGTAAGTCCACA 1260
QY 1261 GAATGGGAGAGGCTTCAATTTGTGCTATCACTCACTCAGACAGAGAAATCCACACA 1320
DB 1261 GAATGGGAGAGGCTTCAATTTGTGCTATCACTCACTCAGACAGAGAAATCCACACA 1320
QY 1321 GGCAGAAACCCGTATTAATGTAAGAGTGTGGAGAGGCTTTCAATTAAGATCGAGCTC 1380
DB 1321 GGCAGAAACCCGTATTAATGTAAGAGTGTGGAGAGGCTTTCAATTAAGATCGAGCTC 1380
QY 1381 GTGAAACATGAGAGATTCATACCGGGGTGAAACCTTATGGGTGACAGATGTGGAG 1440
DB 1381 GTGAAACATGAGAGATTCATACCGGGGTGAAACCTTATGGGTGACAGATGTGGAG 1440
QY 1441 AGCTTTAGTCAAGGACATCAGCTTACACAAATCAGAAAAACGACAGTGGGGCGAAATCC 1500
DB 1441 AGCTTTAGTCAAGGACATCAGCTTACACAAATCAGAAAAACGACAGTGGGGCGAAATCC 1500
QY 1501 TACGAATGTAAAGAGTGGCGGAGAGCATGTAAACAATTAACATCTCCGAGAAACATCAG 1560
DB 1501 TACGAATGTAAAGAGTGGCGGAGAGCATGTAAACAATTAACATCTCCGAGAAACATCAG 1560
QY 1561 AGGATCCACAAAGTTGAAAGAGCTTTTGAACGAGTACCCGCTGTATCTATGTTTC 1620
DB 1561 AGGATCCACAAAGTTGAAAGAGCTTTTGAACGAGTACCCGCTGTATCTATGTTTC 1620
QY 1621 GCTTTCCACAGTTTGTACCTGCAAGTCACTCAGATCAAAATATTAATGAAAAATTC 1680
DB 1621 GCTTTCCACAGTTTGTACCTGCAAGTCACTCAGATCAAAATATTAATGAAAAATTC 1680
QY 1681 CAGAAATTAAGAAATTTTAAGTCTCAATATGTGTGCTTCTGAGTACGCTGTGAATCT 1740
DB 1681 CAGAAATTAAGAAATTTTAAGTCTCAATATGTGTGCTTCTGAGTACGCTGTGAATCT 1740
QY 1741 CTGCGTGTCCGGCTCAGCCGCGCGGAGTGTGAGTCACTCCCTTGTTCAGACATCCAC 1800
DB 1741 CTGCGTGTCCGGCTCAGCCGCGCGGAGTGTGAGTCACTCCCTTGTTCAGACATCCAC 1800
QY 1801 GCGTATACGCAACCAACCTGCTAGTGAAGTGAAGCGCTGTGGTATCAGATCAACT 1860
DB 1801 GCGTATACGCAACCAACCTGCTAGTGAAGTGAAGCGCTGTGGTATCAGATCAACT 1860
QY 1861 ATCCAGACATCAAGTGTCTGTGCCAAGTATCTCATTTTGTCTTAACAGTGGCCCAAG 1920
DB 1861 ATCCAGACATCAAGTGTCTGTGCCAAGTATCTCATTTTGTCTTAACAGTGGCCCAAG 1920
QY 1921 AAGACGAGATGATGATGCTGTGATTCGATATGCAAGAGAACCAAAAGTCTTC 1980

Db 1921 AGAGCAGAGTAGTAGTGTGTTGATTCGGATATGCCAAGAGAGCCACCAAGTCTTC 1980
Qy 1981 CTTTAAATGAAAAGCTGAAAGTTCTCAACTTAA 2015
Db 1981 CTTTAAATGAAAAGTGAAGTTCTCAACTTAA 2015
RESULT 2
AAS03044
ID AAS03044 standard; cDNA, 2098 BP.
XX AAS03044;
AC AAS03044;
XX 29-AUG-2001 (first entry)
DT Human diagnostic and therapeutic (dithp) cDNA sequence #33.
DE Human diagnostic and therapeutic molecule; dithp; gene therapy;
XX thalassemia; cardiovascular disorder; cell proliferative disorder;
KW cancer; neurodegenerative disorder; autoimmune disorder;
KW infectious disorder; inflammatory disorder; developmental disorder;
KW Incyte ID number 9027913dec; transcription factor molecule; ss.
XX Homo sapiens.
OS WO200121836-A2.
XX 29-MAR-2001.
PD 19-SEP-2000; 2000MO-US025643.
PF 23-SEP-1999; 99US-0155760P.
PR 24-SEP-1999; 99US-0155939P.
PR 24-SEP-1999; 99US-0156294P.
PR 28-SEP-1999; 99US-0156565P.
PR 28-SEP-1999; 99US-0156624P.
PR 28-SEP-1999; 99US-0156625P.
PR 24-NOV-1999; 99US-0167410P.
PR 24-NOV-1999; 99US-0167517P.
PR 24-NOV-1999; 99US-0167520P.
PR 24-NOV-1999; 99US-0167521P.
PR 24-NOV-1999; 99US-0167522P.
PR 24-NOV-1999; 99US-0167543P.
PR 24-NOV-1999; 99US-0167543P.
PR 29-NOV-1999; 99US-0167943P.
PR 29-NOV-1999; 99US-0167945P.
PR 30-NOV-1999; 99US-0168197P.
PR 30-NOV-1999; 99US-0168265P.
PR 30-NOV-1999; 99US-0168423P.
PR 30-NOV-1999; 99US-0168432P.
PR 01-DEC-1999; 99US-0168468P.
PR 01-DEC-1999; 99US-0168599P.
PR 02-DEC-1999; 99US-0168611P.
PR 02-DEC-1999; 99US-0168613P.
PR 02-DEC-1999; 99US-0168857P.
XX (INCY-) INCYTE GENOMICS INC.
PA Hodgson DM, Lincoln SE, Russeo PD, Spiro PA, Banville SC;
PI Bratcher SR, Duteour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Greenwalt LB, Panzer SR, Rosberry AM;
PI Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK, Amshay S;
PI Fong WT;
XX WPI; 2001-281607/29.
DR Novel diagnostic and therapeutic polynucleotides, used in disease
PT diagnosis and for gene therapy of conditions such as cancer and
PI thalassemia.
XX Claim 1; Page 271; 299pp; English.
PS The present sequence for human diagnostic and therapeutic (dithp) cDNA
CC

CC sequence #33 is 1 of 71 (AAS03012-AAS03082) novel sequences described in
CC the invention. The present sequence (Incyte ID No: 9027913dec) encodes a
CC transcription factor molecule. The dithp polynucleotides may be used to
CC diagnose a condition disease or disorder associated with human molecules.
CC They can be used to identify the presence of similar nucleic acids. Dithp
CC polynucleotides may be used to generate hybridisation probes for use in
CC chromosomal mapping. Polypeptides (dithp) encoded by dithp are used to
CC screen for molecules which bind to them and modulate their activity.
CC Dithp polynucleotides can be used for gene therapy of disorders such as
CC severe combined immunodeficiency syndrome (SCID), cystic fibrosis,
CC thalassemia, haemophilia resulting from Factor VIII or IX deficiencies,
CC cardiovascular disorders e.g familial hypercholesterolaemia (FH), cell
CC proliferative disorders e.g. cancers, neurodegenerative disorders,
CC autoimmune/inflammatory disorders, infectious disorders and developmental
CC disorders. The antibodies can be used to analyse protein expression
CC levels
XX
SQ Sequence 2098 BP; 610 A; 467 C; 537 G; 484 T; 0 U; 0 Other;
Query Match 98.6%; Score 1986.8; DB 4; Length 2098;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Qy 1 CGCTTTCGACCGGTGACGCAACCGCTGTCTCCGACGTCGCGCAGCGCATCCT 60
Db 85 CGCTTTCGACCGGTGACGCAACCGCTGTCTCCGACGTCGCGCAGCGCATCCT 144
Qy 61 TCAGAAAAAGCATCCCGAGGAGGAGAGCAGATCGTTAAACATCTTAGTCACTTAC 120
Db 145 TCAGAAAAAGCATCCCGAGGAGGAGAGCAGATCGTTAAACATCTTAGTCACTTAC 204
Qy 121 CTTTCGGAATTTGCTTTCTTCAAGTGGAAACCCCGAGAGACATGATCTTTCAGTCT 180
Db 205 CTTTCGGAATTTGCTTTCTTCAAGTGGAAACCCCGAGAGACATGATCTTTCAGTCT 264
Qy 181 AAAACAATGCGCCAGGGGTTTGTGACGTTCCGCGACGATGACATTTCTTCAGAG 240
Db 265 AAAACAATGCGCCAGGGGTTTGTGACGTTCCGCGACGATGACATTTCTTCAGAG 324
Qy 241 GAGTGGCGCTGTGAACTGTCTCAGAGGAGCCTGTACTGGAGCTGATGCTGGAGAC 300
Db 325 GAGTGGCGCTGTGAACTGTCTCAGAGGAGCCTGTACTGGAGCTGATGCTGGAGAC 384
Qy 301 TACAGTAATTGCTGTCTCAGTGGATTTGGAGTGCAGATATGAAAAATTAAGTTTACTACA 360
Db 385 TACAGTAATTGCTGTCTCAGTGGATTTGGAGTGCAGATATGAAAAATTAAGTTTACTACA 444
Qy 361 GAAAAAAACATTCATGAATATAGAGGCTTCCAAAAGAAATTCAGATAGAAAGTAAATCC 420
Db 445 GAAAAAAACATTCATGAATATAGAGGCTTCCAAAAGAAATTCAGATAGAAAGTAAATCC 504
Qy 421 CTGGCGGTAACTGATATGTGAAGGTAAGCTTGAAGACCAAGCGCTTCAAGAGGAGG 480
Db 505 CTGGCGGTAACTGATATGTGAAGGTAAGCTTGAAGACCAAGCGCTTCAAGAGGAGG 564
Qy 481 TATGTCATCAGATGATATCAATTAATGTCAAAAGGCTGTACTATGAGAGGACCC 539
Db 565 TATGTCATCAGATGATATCAATTAATGTCAAAAGGCTGTACTATGAGAGGACCC 624
Qy 540 TCTTAGAACATCAGAGACATCATTAAGAGAAATTCCTTGAATGTAAGACTGTGGGAA 599
Db 625 TCTTAGAACATCAGAGACATCATTAAGAGAAATTCCTTGAATGTAAGACTGTGGGAA 684
Qy 600 GGCCTTAGTGTGTGCTATCAACTTAGTCAACATCAGAAAAATTCATCTGTGAGAAAC 659
Db 685 GGCCTTAGTGTGTGCTATCAACTTAGTCAACATCAGAAAAATTCATCTGTGAGAAAC 744
Qy 660 TTATGAATGTAAGAAATTAAGAGGCTTCCGTTGGGCGAATAGCTTACTCAATCA 719
Db 745 TTATGAATGTAAGAAATTAAGAGGCTTCCGTTGGGCGAATAGCTTACTCAATCA 804
Qy 720 AAAAATTCTACTGGGAGAGCCCTTACGAATGTAAAGACTGTGGAGAGGCTTTTCAGATG 779

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Db      805 AAAAAATCACTGCGGAGAGAGCCCTACGATGTAAAGA CTGTGGAGAGGCTTTTCGATG 864
Qy      760 GGGCTCAAGCCTCGTTATTCATAGAGATTCATCT -GATGAAAAAACCTTAATGATGA 838
Db      865 GGGCTCAAGCCTCGTTATTCATAGAGATTCATCT GGGGTGAAAAACCTTTAATGATGA 924
Qy      839 AAGACTGTGGAAAGGCTTTGCGCGGTGTATGAGCTCACTAGCACCGAGAGATTCACA 898
Db      925 AAGACTGTGGAAAGGCTTTGCGCGGTGTATGAGCTCACTAGCACCGAGAGATTCACA 984
Qy      899 CTGGGGAGAAACATACGAATGCAAAAGACTGTGGAGAGCCTTTAGCCCTGTGTATTAAC 958
Db      985 CTGGGGAGAAACATACGAATGCAAAAGACTGTGGAGAGCCTTTAGCCCTGTGTATTAAC 1044
Qy      959 TTATTCAGACAGAGAAATTCATAGTGGGAGAGAGCCTTACGATGTAAAGA CTGTGGGA 1018
Db      1045 TTATTCAGACAGAGAAATTCATAGTGGGAGAGAGCCTTACGATGTAAAGA CTGTGGGA 1104
Qy      1019 AGGCTTTTATTTGTGGTTCAGGCTTCATT CAGCATMAAAGAAATTCACACAGGTGAGAAAC 1078
Db      1105 AGGCTTTTATTTGTGGTTCAGGCTTCATT CAGCATMAAAGAAATTCACACAGGTGAGAAAC 1164
Qy      1079 CCTATGAATGTCAAGAAATGTGGAGAGGCTTTACTGAGATCAATTCCTTACTCAGATC 1138
Db      1165 CCTATGAATGTCAAGAAATGTGGAGAGGCTTTACTGAGATCAATTCCTTACTCAGATC 1224
Qy      1139 AGAAGATCCACACCGGTGAGAAAGCCTCACGAATGTAAAGAGTGTGGAGAGGCTTCGCT 1198
Db      1225 AGAAGATCCACACCGGTGAGAAAGCCTCACGAATGTAAAGAGTGTGGAGAGGCTTCGCT 1284
Qy      1199 GGGGTTTCGAGCCTCGTTAAGACGAGAGAGATACATACGCGGCGAGAAAGCCTTACAGTGA 1258
Db      1285 GGGGTTTCGAGCCTCGTTAAGACGAGAGAGATACATACGCGGCGAGAAAGCCTTACAGTGA 1344
Qy      1259 CAGAAATGTGGAGAGGCTTCATATGTGCTATACCTCACTCAGACGAGAGAAATCCACA 1318
Db      1345 CAGAAATGTGGAGAGGCTTCATATGTGCTATACCTCACTCAGACGAGAGAAATCCACA 1404
Qy      1319 CAGGCGAAACCCCGTAAATGTAAAGAGTGTGGAGAGGCTTCATTTATGATCGAGCC 1378
Db      1405 CAGGCGAAACCCCGTAAATGTAAAGAGTGTGGAGAGGCTTCATTTATGATCGAGCC 1464
Qy      1379 TCGTGAAACATGAGAGAAATTCATACCGGGGTGAAACCTTAATGGGTGTACAGAAATGTGGGA 1438
Db      1465 TCGTGAAACATGAGAGAAATTCATACCGGGGTGAAACCTTAATGGGTGTACAGAAATGTGGGA 1524
Qy      1439 AAGAGCTTTAGTCAAGCGCCATCAGCTTACACATACGAGAAAGCAGACAGTGGGGCCAAAT 1498
Db      1525 AAGAGCTTTAGTCAAGCGCCATCAGCTTACACATACGAGAAAGCAGACAGTGGGGCCAAAT 1584
Qy      1499 CCTACGAATGTAAAGAGTGTGGAGAGGAGCATGTAAACCACTTAACCACTTCCGAGAACATC 1558
Db      1585 CCTACGAATGTAAAGAGTGTGGAGAGGAGCATGTAAACCACTTAACCACTTCCGAGAACATC 1644
Qy      1559 AAGAGATCCACACAGTGAAGAGCCTTTTGAACGAGTAGCCGCTCGTATCTATGTT 1618
Db      1645 AAGAGATCCACACAGTGAAGAGCCTTTTGAACGAGTAGCCGCTCGTATCTATGTT 1704
Qy      1619 TCGCTTTCCACAGATTGTATACCTGAGTCAACCTGCAAGTTCAAAAAATTTAAATGAGAAAT 1678
Db      1705 TCGCTTTCCACAGATTGTATCTGCAAGTCAACCTGCAAGTTCAAAAAATTTAAATGAGAAAT 1764
Qy      1679 TCCAGAAATTAAGAAATTTTAAAGTCTCAAAATGTGTGCCCTTCTGAGTAGCGGTATGAAT 1738
Db      1765 TCCAGAAATTAAGAAATTTTAAAGTCTCAAAATGTGTGCCCTTCTGAGTAGCGGTATGAAT 1824
Qy      1739 CTCTCGCTGTCCGGCTTCAGCCGCGCGGGAGTGTAGTCAATCCCTTGTGTCCAGACATCC 1798
Db      1825 CTCTCGCTGTCCGGCTTCAGCCGCGCGGGAGTGTAGTCAATCCCTTGTGTCCAGACATCC 1884
Qy      1799 AGGCTGTATACGCCACCCCTGCTAGTACTTAAGCCGCTTGTGTGTATCAATCA 1858
Db      1885 AGGCTGTATACGCCACCCCTGCTAGTACTTAAGCCGCTTGTGTGTATCAATCA 1944

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Qy      1859 CTATCCAGCATCAGTGCCTGTGCCCCAAGTAGTCTTCACTTTGCTTAAACAGTGGCCCC 1918
Db      1945 CTATCCAGCATCAGTGCCTGTGCCCCAAGTAGTCTTCACTTTGCTTAAACAGTGGCCCC 2004
Qy      1919 AGAGAGCAGAGTAGTGTCTGTGTGATTCGGATATGCCAAAGAGAGAGCCACAAAGTGCT 1978
Db      2005 AGAGAGCAGAGTAGTGTGTGTGTGATTCGGATATGCCAAAGAGAGAGCCACAAAGTGCT 2064
Qy      1979 TCCCTTTAAATGAAAGGAGGAGTTCTCAACTT 2012
Db      2065 TCCCTTTAAATGAAAGGAGGAGTTCTCAACTT 2098

RESULT 3
ABA82974
ID   ABA82974 standard; DNA; 2173 BP.
XX
XX   ABA82974;
AC   XX
XX   05-FEB-2002 (first entry)
DT   XX
DE   Human transcription factor TRFX-1 coding sequence.
XX
XX   Human; transcription factor; TRFX; cell proliferative disease;
KW   autoimmune disease; inflammation; neurological disease;
KW   developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
KW   neuroprotective; antiinflammatory; gene therapy; db.
XX
XX   Homo sapiens.
OS   XX
XX   WO200172777-A2.
PN   XX
XX   04-OCT-2001.
PD   XX
PF   13-MAR-2001; 2001WO-US008117.
PR   XX
PR   13-MAR-2000; 2000US-0186986P.
PA   (INCYTE) INCYTE GENOMICS INC.
XX
XX   Hillman JL, Baughn WR, Yue H, Lal P, Lu DM, Patterson C;
PI   Azimzal Y, Bandman O, Tang YT, Matchur P, Shah P, Au-Young J;
PI   Reddy R;
XX
XX   MPI: 2001-570896/64.
DR   P-PSDB; ABB50150.
DR
PT   Novel transcription factor polypeptides, used to treat diseases
PT   associated with altered activity and expression of TRFX, and to screen
PT   for agents capable of modulating its activity.
XX
XX   Claim 11; Page 252; 327pp; English.
PS
XX
XX   The present sequence is the coding sequence for a human transcription
CC   factor. The transcription factor and its coding sequence are useful in
CC   the diagnosis, treatment and prevention of diseases associated with
CC   altered expression of the transcription factor e.g. cell proliferative,
CC   autoimmune/inflammatory, neurological and developmental disorders. A
CC   number of specific disorders/diseases are given in the specification,
CC   including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
CC   allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic
CC   dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,
CC   Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,
CC   psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative
CC   colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC   disease, stroke, and viral, bacterial, fungal and protozoal infections
XX
XX   Sequence 2173 BP; 648 A; 482 C; 555 G; 488 T; 0 U; 0 Other;
SQ

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Query Match      97.6%; Score 1967.4; DB 5; Length 2173;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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47 CAGCCAGATCCTTCAGAAAAAGCATCCCGAGGAGAGAGAGCATGCTTAACATCTT 106
189 CAGGCCAGATCTTTCAGAAAAAGCATCCCGAGGAGAGAGAGCATGCTTAACATCTT 248
107 AGGTGAGCTAGACCTCTCGAATTTGCTTCTTCAGTGAAGACCCCGAGAGACTGATC 166
249 AGGTGAGCTAGACCTCTCGAATTTGCTTCTTCAGTGAAGACCCCGAGAGACTGATC 308
167 AGTTCCTTCACTTAAACATATGAGCCAGAGGTTTGTGATGCTTCCGCGAGCTGATAG 226
309 AGTTCCTTCACTTAAACATATGAGCCAGAGGTTTGTGATGCTTCCGCGAGCTGATAG 368
227 ACTTTTCAGGAGAGAGGAGGCTGTCTGAACTCTGCTCAGAGGAGACCTGTGCTGAGAG 286
369 ACTTTTCAGGAGAGAGGAGGCTGTCTGAACTCTGCTCAGAGGAGACCTGTGCTGAGAG 428
287 TGATGCTGAGAGACTTACAGTAACTTGTCTCACTGGAATTTGGAGTCAAGCATATGAATA 346
429 TGATGCTGAGAGACTTACAGTAACTTGTCTCACTGGAATTTGGAGTCAAGCATATGAATA 488
347 AGAGTTTACCTTACAGAAAAAAACATTTCATGAATAAGGCTTCCAAAAGAAATTCAGATA 406
489 AGAGTTTACCTTACAGAAAAAAACATTTCATGAATAAGGCTTCCAAAAGAAATTCAGATA 548
407 GAGAGAGTAAATCCCTTGCCGCTAATGATATGTAAGGTAAGCTTGAAACACACAGC 466
549 GAGAGAGTAAATCCCTTGCCGCTAATGATATGTAAGGTAAGCTTGAAACACACAGC 608
467 GCTCCAGAGGAGATGATCATCATGATGATCATCAATTAATGCTCAAAAAGGCTGCTACTA 526
609 GCTCCAGAGGAGATGATGATCATCATGATGATCATCAATTAATGCTCAAAAAGGCTGCTACTA 668
527 GAGAGAGCAACCCCTCTCTAGAACATCATCAGAGACATCATTAAGAGAAATTCCTTGAATGTA 586
669 GAGAGAGCAACCCCTCTCTAGAACATCATCAGAGACATCATTAAGAGAAATTCCTTGAATGTA 728
587 AGAGATGAGGAGAGGCTTTTGTAGTCTGTGCTATCACTTAATGTAACATCAAAAAATTCCTA 646
729 AGAGATGAGGAGAGGCTTTTGTAGTCTGTGCTATCACTTAATGTAACATCAAAAAATTCCTA 788
647 CTGTGAGAAAACTTATGATATGTAAGAAATGTAAGAGGCTTCCGTTGGGGCAATCAAGC 706
789 CTGTGAGAAAACTTATGATATGTAAGAAATGTAAGAGGCTTCCGTTGGGGCAATCAAGC 848
707 TTAATCAACATCAAAAAATTCATCTGAGGAGAGACCCCTTACGAATGTAAAGACTGTGAG 766
849 TTAATCAACATCAAAAAATTCATCTGAGGAGAGACCCCTTACGAATGTAAAGACTGTGAG 908
767 AGGCTTTTCAGATGAGGCTCAAGCCCTGTTATTCATTAAGAGATTCATTAATGTAAGAAAC 826
909 AGGCTTTTCAGATGAGGCTCAAGCCCTGTTATTCATTAAGAGATTCATTAATGTAAGAAAC 968
827 CCTATGATGTAAGAGACTGTGAGAAAGGCTTCCGCGTGTGATGAGCTCACTCAGACCC 886
969 CCTATGATGTAAGAGACTGTGAGAAAGGCTTCCGCGTGTGATGAGCTCACTCAGACCC 1028
887 AGAGATTCACACATGAGGAGAAAGACTTACGAATGCAAAAGACTGTGAGAAAGACTTTAGCC 946
1029 AGAGATTCACACATGAGGAGAAAGACTTACGAATGCAAAAGACTGTGAGAAAGACTTTAGCC 1088
947 GTGTCTAATAAATTTCAGACCAAGAGAAATTCATTAAGTGGGAGAGACCTTACAGATGTA 1006
1089 GTGTCTAATAAATTTCAGACCAAGAGAAATTCATTAAGTGGGAGAGACCTTACAGATGTA 1148
1007 AAGACTGTGAGAAAGGCTTTTATTTGTGTTCAAGGCTCATTCAGCATTAAGAAATTCACA 1066
1149 AAGACTGTGAGAAAGGCTTTTATTTGTGTTCAAGGCTCATTCAGCATTAAGAAATTCACA 1208
1067 CAGGTGAGAAACCTTATGATATGTAAGAAATGTAAGTGGAGAGGCTTTTCTGAGTCAATTAAC 1126
1209 CAGGTGAGAAACCTTATGATATGTAAGAAATGTAAGTGGAGAGGCTTTTCTGAGTCAATTAAC 1268

QY 1127 TTAATCAGATCAGAGATTCACACCGGTGAGAAAGCTTCAAGATGTAAGAGTGGGA 1186
Db 1269 TTAATCAGATCAGAGATTCACACCGGTGAGAAAGCTTCAAGATGTAAGAGTGGGA 1328
QY 1187 AGGCTTTTCGCTGGGTTTCAGACCTCTGTTAAGCAGAGAGTACATACGGGCGAAGAC 1246
Db 1329 AGGCTTTTCGCTGGGTTTCAGACCTCTGTTAAGCAGAGAGTACATACGGGCGAAGAC 1388
QY 1247 CGTACAGTGCACAGAAATGTGGAAAGGCTTCAATTTGTGCTATCACTCACTCAGACG 1306
Db 1389 CGTACAGTGCACAGAAATGTGGAAAGGCTTCAATTTGTGCTATCACTCACTCAGACG 1448
QY 1307 AGAGATTCACACAGGCGAAACCCGCTAATAATGTAAGAGTGGAGAGCTTCAATT 1366
Db 1449 AGAGATTCACACAGGCGAAACCCGCTAATAATGTAAGAGTGGAGAGCTTCAATT 1508
QY 1367 ATGATTCAGGCTCTGTGAAACATGAGAAATTCATACCGGGTGAACCTTATGGGTGA 1426
Db 1509 ATGATTCAGGCTCTGTGAAACATGAGAAATTCATACCGGGTGAACCTTATGGGTGA 1568
QY 1427 CAGAAATGTGGAGAGCTTTTATGTCACGGCATCAGCTTACACATCAAGAAAGCACA 1486
Db 1569 CAGAAATGTGGAGAGCTTTTATGTCACGGCATCAGCTTACACATCAAGAAAGCACA 1628
QY 1487 GTGGGGCGAAATCCTACGAATGTAAAGAGTGGGAGAGGCAATGTAAACACCTTAACATC 1546
Db 1629 GTGGGGCGAAATCCTACGAATGTAAAGAGTGGGAGAGGCAATGTAAACACCTTAACATC 1688
QY 1547 TCCGAGAACATCAGAGATTCACACACAGTTGAAGAGCTTTTGAAGCAGTAGCCGCTC 1606
Db 1689 TCCGAGAACATCAGAGATTCACACACAGTTGAAGAGCTTTTGAAGCAGTAGCCGCTC 1748
QY 1607 GTATCTATGTTTGGCTTTCCACAGTTTGTATCTGACATCACTGACCTTCAAAATAT 1666
Db 1749 GTATCTATGTTTGGCTTTCCACAGTTTGTATCTGACATCACTGACCTTCAAAATAT 1808
QY 1667 TAAATGAAAAATTCAGAAATTAAGAAATTTTAAGTCTAAATGTGTCCTTTCAGATA 1726
Db 1809 TAAATGAAAAATTCAGAAATTAAGAAATTTTAAGTCTAAATGTGTCCTTTCAGATA 1868
QY 1727 GCGTATGAAATCTCTCGCTGTCCGCTCCAGCCGCGGGAGTGTGATCATCCCTTGG 1786
Db 1869 GCGTATGAAATCTCTCGCTGTCCGCTCCAGCCGCGGGAGTGTGATCATCCCTTGG 1928
QY 1787 TCCAGCATCATCAGCTGTATACGCCACACACCTGCTAGTGAATTAAGTACCTTGG 1846
Db 1929 TCCAGCATCATCAGCTGTATACGCCACACACCTGCTAGTGAATTAAGTACCTTGG 1988
QY 1847 TGATCAGATCAACTATCCAGCATTCAGAGTGCCTGTGCCAAAGTATGTCCTCACTTGGCTT 1906
Db 1989 TGATCAGATCAACTATCCAGCATTCAGAGTGCCTGTGTGCCAAAGTATGTCCTCACTTGGCTT 2048
QY 1907 AACAGTGGCCCAAGAGACAGAGATGATGCTGTGATTCGATATGCAAGAGAG 1966
Db 2049 AACAGTGGCCCAAGAGACAGAGATGATGCTGTGATTCGATATGCAAGAGAG 2108
QY 1967 CCACAAAGTCTCTCTTTTAAATGAAAAAGTGAAGTTTCACTTAA 2015
Db 2109 CCACAAAGTCTCTCTTTTAAATGAAAAAGTGAAGTTTCACTTAA 2157

RESULT 4
AAK94562 standard; cDNA; 2169 BP.
ID AAK94562;
XX AAK94562;
AC AAK94562;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human full-length cDNA, SEQ ID NO: 3469.
DE Human full-length cDNA; cDNA synthesis; oligo-capping; ss.
XX
XX

OS Homo sapiens.
 XX
 PN EPI130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR P-PSDB; AAM93629.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX
 PS Claim 8; SEQ ID NO 3469; 1380bp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a full length human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in CD-ROM format directly
 CC from EPO
 XX
 SQ Sequence 2169 BP; 633 A; 485 C; 560 G; 491 T; 0 U; 0 Other;

Query Match 97.2%; Score 1958; DB 4; Length 2169;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 47 CAGGCCAGCATCTCTGAGAAAAAGCATCCCGAGAGAGAAAGCAATCGTTAAACATCTT 106
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 QY 167 AGTCTTCAGTTCTTAAACAATGAGGCCAGGTTTGTGACGTTGCCGAGAGTACGCAATG 226
 DB 324 AGTCTTCAGTTCTTAAACAATGAGGCCAGGTTTGTGACGTTGCCGAGAGTACGCAATG 383
 QY 227 ACTTCTCTGAGAGAGTGGGCTGTCTGAACCTGTCTGAGAGGACCTGTACTGGGAGG 286
 DB 384 ACTTCTCTGAGAGAGTGGGCTGTCTGAACCTGTCTGAGAGGACCTGTACTGGGAGG 443
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 XX ADL31436;
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 DT 20-MAY-2004 (first entry)
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 DE Full length human cDNA clone Segid 3469.
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 KW human; medicine; signal transduction; glycoprotein; transcription;
 KM oligo-capping method; seq; gene.
 XX
 OS Homo sapiens.
 XX
 PN EP1396543-A2.
 XX
 PD 10-MAR-2004.
 PF 07-JUL-2000; 2003EP-00025638.
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 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Ota T, Nishikawa T, Isegai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR F-PSDB; ADL31437.
 XX
 PT WPI; 2004-204755/20.
 XX
 PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 length human cDNAs.
 PS Example 1; SEQ ID NO 3469; 1340pp; English.
 XX
 CC This invention relates to a novel primers useful for synthesizing full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/

CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polynucleotide sequence is a
 CC full length human cDNA clone of the invention.
 XX
 SQ Sequence 2169 BP; 633 A; 485 C; 560 G; 491 T; 0 U; 0 Other;
 Query Match 97.2%; Score 1958; DB 12; Length 2169;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 47 CAGGCCAGATCTCTTCAAGAAAAGCATCCCGAGAGAGAAAGCAATGCTTAACTTT 106
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RESULT 6
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ID AAS25944 standard; cDNA; 3293 BP.
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AC AAS25944;
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DT 07-NOV-2001 (first entry)
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DE Human cDNA encoding a novel secreted protein, Seq ID 123.
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KW Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytosolic;
KW cardiant; vasotropic; cerebroprotective; neuroprotective;
KW antibacterial; virucide; fungicide; opthalmological; vulnerrary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN MO200155322-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001341.
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PR 31-JUN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 22-AUG-2000; 2000US-022681P.
PR 22-AUG-2000; 2000US-022688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
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PR 05-SEP-2000; 2000US-0229513P.
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PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.


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Db 1876 TTAGTAGCCGCTGTGTGTATCAGATCAATATCCAGATCAACAGTCCGTGAGCCAGAT 1935
QY 1891 AGTCTCACTTGTCTTAAACAGTGGCCCGAGAGACAGAGTGTGATGCTGTGATTCG 1950
    |||
Db 1936 AGTCTCACTTGTCTTAAACAGTGGCCCGAGAGACAGAGTGTGATGCTGTGATTCG 1995
QY 1951 ATATGCCAAAGAGAGCCCAAAAGTCTCTTTTAAAGAAAGGTGAAAGTTCACAC 2010
    |||
Db 1996 ATATGCCAAAGAGAGCCCAAAAGTCTCTTTTAAAGAAAGGTGAAAGTTCACAC 2055
QY 2011 TTTAAA 2015
    |||
Db 2056 TTTAAA 2060

```

```

RESULT 7
ABX73285
ID ABX73285 standard; DNA; 3293 BP.
XX
AC ABX73285;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human novel polynucleotide #113.
XX
KW Human; gene; ds; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disease; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotoxic; cytostatic; antiallergic; thrombolytic;
KW haemostatic; antiarteriosclerotic.

```

XX OS Homo sapiens.
XX FN US2002132753-A1.
XX PD 19-SEP-2002.
XX PE 17-JAN-2001; 2001US-00764864.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 28-JUN-2000; 2000US-0214866P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 11-JUL-2000; 2000US-0217496P.
XX PR 14-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225267P.
XX PR 14-AUG-2000; 2000US-0225270P.
XX PR 14-AUG-2000; 2000US-0225447P.
XX PR 14-AUG-2000; 2000US-0225757P.
XX PR 14-AUG-2000; 2000US-0225758P.
XX PR 22-AUG-2000; 2000US-0226868P.
XX PR 30-AUG-2000; 2000US-0228924P.
XX PR 01-SEP-2000; 2000US-0229287P.
XX PR 01-SEP-2000; 2000US-0229343P.
XX PR 01-SEP-2000; 2000US-0229344P.
XX PR 01-SEP-2000; 2000US-0229345P.
XX PR 05-SEP-2000; 2000US-0229509P.
XX PR 05-SEP-2000; 2000US-0229513P.
XX PR 08-SEP-2000; 2000US-0231413P.
XX PR 21-SEP-2000; 2000US-0234223P.
XX PR 21-SEP-2000; 2000US-0234274P.
XX PR 25-SEP-2000; 2000US-0234977P.
XX PR 27-SEP-2000; 2000US-0235834P.
XX PR 29-SEP-2000; 2000US-0236327P.
XX PR 29-SEP-2000; 2000US-0236367P.
XX PR 29-SEP-2000; 2000US-0236368P.
XX PR 29-SEP-2000; 2000US-0236369P.
XX PR 29-SEP-2000; 2000US-0236370P.
XX PR 02-OCT-2000; 2000US-0236802P.
XX PR 02-OCT-2000; 2000US-0237037P.
XX PR 02-OCT-2000; 2000US-0237038P.
XX PR 02-OCT-2000; 2000US-0237039P.
XX PR 02-OCT-2000; 2000US-0237040P.
XX PR 13-OCT-2000; 2000US-0239335P.
XX PR 20-OCT-2000; 2000US-0240960P.
XX PR 20-OCT-2000; 2000US-0241785P.
XX PR 20-OCT-2000; 2000US-0241809P.
XX PR 01-NOV-2000; 2000US-0244617P.
XX PR 17-NOV-2000; 2000US-0249299P.
XX PR 08-DEC-2000; 2000US-0251856P.
XX PR 08-DEC-2000; 2000US-0251868P.
XX PR 08-DEC-2000; 2000US-0251869P.
XX PA (ROSE/) ROSEN C A.
XX PA (RUBE/) RUBEN S M.
XX PA (BARA/) BARASH S C.
XX PI Rosen CA, Ruben SM, Barash SC;
XX DR MPI: 2003-147444/14.
XX P-PSDB: ABUS5025.
XX PT New polypeptides and nucleic acids, useful in gene therapy for treating,
XX PT inhibiting or preventing e.g. neural, immune system, muscular,
XX PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
XX PT renal disorders.

XX PS Claim 1; SEQ ID NO 123; 402bp; English.
XX CC The invention relates to human novel polypeptides and their associated
XX CC polynucleotides. The polypeptides and polynucleotides are useful in gene
XX CC therapy for treating, inhibiting or preventing neural disorders, immune
XX CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
XX CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
XX CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
XX CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
XX CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
XX CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
XX CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
XX CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
XX CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
XX CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
XX CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
XX CC human novel polynucleotides of the invention
SQ Sequence 3293 BP; 974 A; 717 C; 750 G; 852 T; 0 U; 0 Other;

Query Match 96.6%; Score 1946.2; DB 8; Length 3293;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 3; Indels 32; Gaps 3;

QY 1 CGCTTTCACCCGTCGACGCAACCGCTGTCTCCGCCATGCCGCGCAGCATCTCT 60
DB CGCTTTCGACCCGTCGACGCAACCGCTGTCTCCGCCATGCCGCGCAGCATCTCT 77
QY 61 TCAGAAAAGCATCCCGAGGAGGAAGCAATGTTAAATCTCTAGTCTC----- 111
DB TCAGAAAAGCATCCCGAGGAGGAAGCAATGTTAAATCTCTAGTCTC----- 137
QY 78 TCAGAAAAGCATCCCGAGGAGGAAGCAATGTTAAATCTCTAGTCTC----- 151
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 197
QY 138 AGTAGGAAACCGACACTGTGAGGCTTAGCTTCGGAATTTGTTCTTTCAGTGAAGAAC 197
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 210
QY 151 CCCGAGGAAGCTGATCACTTCTTCACTTCTTCAAAACATGCGCCGAGGTTTGGTACCTTC 210
DB CCCGAGGAAGCTGATCACTTCTTCACTTCTTCAAAACATGCGCCGAGGTTTGGTACCTTC 257
QY 211 GCCGACGTAGCAATAGACTTTTCTCAGAGGAGTGGGCTGTCTGAACTCTGCTCAGAGG 270
DB GCCGACGTAGCAATAGACTTTTCTCAGAGGAGTGGGCTGTCTGAACTCTGCTCAGAGG 317
QY 258 GCCGACGTAGCAATAGACTTTTCTCAGAGGAGTGGGCTGTCTGAACTCTGCTCAGAGG 317
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 330
QY 271 GACCTGTACTGGAGCGTGATCTGGAGAACTTACAGTAACTTGTCTCACTGGATTGGAG 330
DB GACCTGTACTGGAGCGTGATCTGGAGAACTTACAGTAACTTGTCTCACTGGATTGGAG 377
QY 318 GACCTGTACTGGAGCGTGATCTGGAGAACTTACAGTAACTTGTCTCACTGGATTGGAG 377
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 437
QY 331 TCAGCATATGAAAATTAAGAGTTTACCTTACAGAAAACATTCATGAATAAGGCTTCC 390
DB TCAGCATATGAAAATTAAGAGTTTACCTTACAGAAAACATTCATGAATAAGGCTTCC 437
QY 378 TCAGCATATGAAAATTAAGAGTTTACCTTACAGAAAACATTCATGAATAAGGCTTCC 437
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 450
QY 391 AAAAGGAATTCAGATAGAGAAAGTAAATCCCTTGGCCGTTAATGGATATGGAAGTACG 450
DB AAAAGGAATTCAGATAGAGAAAGTAAATCCCTTGGCCGTTAATGGATATGGAAGTACG 497
QY 438 AAAAGGAATTCAGATAGAGAAAGTAAATCCCTTGGCCGTTAATGGATATGGAAGTACG 497
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 510
QY 451 CTTGAAAGACCAAGCGCTCCAGAGGAGTATGTCAATCAGATGATCATTAATTATTC 510
DB CTTGAAAGACCAAGCGCTCCAGAGGAGTATGTCAATCAGATGATCATTAATTATTC 556
QY 498 CTTGAAAGACCAAGCGCTCCAGAGGAGTATGTCAATCAGATGATCATTAATTATTC 556
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 570
QY 511 AAAAGGCTCTGCTACTAGAGAAAGCAACCCCTCTTGAACAATCAGAGCATCATTAAGAG 570
DB AAAAGGCTCTGCTACTAGAGAAAGCAACCCCTCTTGAACAATCAGAGCATCATTAAGAG 616
QY 557 AAAAGGCTCTGCTACTAGAGAAAGCAACCCCTCTTGAACAATCAGAGCATCATTAAGAG 616
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 630
QY 571 AATTCCTTGAATGTAAGAGCTGTGGAAAGGCTTATGTCGAGTCACTTAAGTCA 630
DB AATTCCTTGAATGTAAGAGCTGTGGAAAGGCTTATGTCGAGTCACTTAAGTCA 676
QY 617 AATTCCTTGAATGTAAGAGCTGTGGAAAGGCTTATGTCGAGTCACTTAAGTCA 676
DB -----AGCTTAGCCTTCGAAATTTGTTCTTTCAGTGAAGAAC 690
QY 631 CATCAGAAATTCATCTACTGTGTGAGAAACCTTATGAATGAATGAATGAAGAGGCTTTC 690
DB CATCAGAAATTCATCTACTGTGTGAGAAACCTTATGAATGAATGAATGAAGAGGCTTTC 736


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QY 691 CGTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTGGGGAGAAAGCCCTTACGAA 750
    |||||
DB 737 CGTTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATCTGGGGAGAAAGCCCTTACGAA 796
    |||||
QY 751 TGTAAAGACTGTGGGAGAGGCTTTTGCATGGGGCTCAAGCTCGTTATTTGATTAAGAGAT 810
    |||||
DB 797 TGTAAAGACTGTGGGAGAGGCTTTTGCATGGGGCTCAAGCTCGTTATTTGATTAAGAGAT 856
    |||||
QY 811 CATTAAGTGTAAAAAACCCTATGATGTAAAAAGACTGTGAAAAAGGCTTTGCGCGTGTGAT 870
    |||||
DB 857 CATACTCG--GAAAAACCCTATGATGTAAAAAGACTGTGAAAAAGGCTTTGCGCGTGTGAT 915
    |||||
QY 871 GAGCTCACTCAGCAGCAGAGATTCCA CACTGGGAGAAAAAGACTGATGCAAAAGACTGT 930
    |||||
DB 916 GAGCTCACTCAGCAGCAGAGATTCCA CACTGGGAGAAAAAGACTGATGCAAAAGACTGT 975
    |||||
QY 931 GGGAAAGACCTTTAGCCGTGTGTATTAACCTATTCACACAAAGAAATTCATAGTGGGGAG 990
    |||||
DB 976 GGGAAAGACCTTTAGCCGTGTGTATTAACCTATTCACACAAAGAAATTCATAGTGGGGAG 1035
    |||||
QY 991 AAGCCTTACGAGTGTAAAAAGACTGTGGGAAAGGCTTTTATTTGTGTTCAAGCCTCATTTAG 1050
    |||||
DB 1036 AAGCCTTACGAGTGTAAAAAGACTGTGGGAAAGGCTTTTATTTGTGTTCAAGCCTCATTTAG 1095
    |||||
QY 1051 CATAAAAAGATTCAACAAGGTGAGAAACCCTATGAAATGTCAAGAAATGTGGAAAGGCTTTT 1110
    |||||
DB 1096 CATAAAAAGATTCAACAAGGTGAGAAACCCTATGAAATGTCAAGAAATGTGGAAAGGCTTTT 1155
    |||||
QY 1111 ACTCGAGTCAATTAACCTTACTGAGCATCAAGAAATTCACACCGGTGAGAAAGCCTTCACGAA 1170
    |||||
DB 1156 ACTCGAGTCAATTAACCTTACTGAGCATCAAGAAATTCACACCGGTGAGAAAGCCTTCACGAA 1215
    |||||
QY 1171 TGTAAAGAGTGTGGGAAAGGCTTTGCGTGGGGTTCAGACCTCGTTAAGCAGAGAGATTA 1230
    |||||
DB 1216 TGTAAAGAGTGTGGGAAAGGCTTTGCGTGGGGTTCAGACCTCGTTAAGCAGAGAGATTA 1275
    |||||
QY 1231 CATACGGGCGAGAAAGCCGTACAAATGTGAGCAAGAAATGTGGGAAAGCCTTCAATTTGTGCTAT 1290
    |||||
DB 1276 CATACGGGCGAGAAAGCCGTACAAATGTGAGCAAGAAATGTGGGAAAGCCTTCAATTTGTGCTAT 1335
    |||||
QY 1291 CACCTCACTCAGACGAGAAATCCACAGCGGAGAAACCCCGTAAATGTAAGAGATGT 1350
    |||||
DB 1336 CACCTCACTCAGACGAGAAATCCACAGCGGAGAAACCCCGTAAATGTAAGAGATGT 1395
    |||||
QY 1351 GGGAAAGGCTTTCAATTAATGTGATGAGGCTCGTGAACAATGAGAGAAATTCATACCGGGGTG 1410
    |||||
DB 1396 GGGAAAGGCTTTCAATTAATGTGATGAGGCTCGTGAACAATGAGAGAAATTCATACCGGGGTG 1455
    |||||
QY 1411 AAACCTATGGTGTACAGAAATGTGGGAAAGGCTTTAGTCACGCGCATCAGCTTACACAA 1470
    |||||
DB 1456 AAACCTATGGTGTGTACAGAAATGTGGGAAAGGCTTTAGTCACGCGCATCAGCTTACACAA 1515
    |||||
QY 1471 CATCAAAAAACGACAGTGGGGGAGAAATCTTAAGAAATGTAAAGAGTGGGAAAGGATGT 1530
    |||||
DB 1516 CATCAAAAAACGACAGTGGGGGAGAAATCTTAAGAAATGTAAAGAGTGGGAAAGGATGT 1575
    |||||
QY 1531 AACCACTTAACCATCTCCGAGAACATCAGAGATTCACAAACAGTTGAAGGCTTTTGA 1590
    |||||
DB 1576 AACCACTTAACCATCTCCGAGAACATCAGAGATTCACAAACAGTTGAAGGCTTTTGA 1635
    |||||
QY 1591 ACGCAGTAGCCGCTCGTATCTATGTTTGCCTTTCCACAGTTTGTATCTGACAGTCAAC 1650
    |||||
DB 1636 ACGCAGTAGCCGCTCGTATCTATGTTTGCCTTTCCACAGTTTGTATCTGACAGTCAAC 1695
    |||||
QY 1651 TGTAGTTCAAAAAATTTAAATGTGAAAAATTCAGAAAAAAGAAATTTTAACTTCAATGG 1710
    |||||
DB 1696 TGTAGTTCAAAAAATTTAAATGTGAAAAATTCAGAAAAAAGAAATTTTAACTTCAATGG 1755
    |||||
QY 1711 TGTGACCTTGTAGTAGCAGTGAATCTCGCTGTCCGGCTCCAGCCGCGCGGGAGAT 1770
    |||||
DB 1756 TGTGACCTTGTAGTAGCAGTGAATCTCGCTGTCCGGCTCCAGCCGCGCGGGAGAT 1815
    |||||
QY 1771 GTGAGTCAATCCCTTGTGTCAAGACATCAAGCTGTATAGCCACCACTGTCTAGTAC 1830
    |||||
```

```
DB 1816 GTGAGTCAATCCCTTGTGTCAAGACATCAAGCTGTATAGCCACCACTGTCTAGTAC 1875
    |||||
QY 1831 TTAGTAGCCGCTTTGTGATTCAGATCAACTATCCAGCATCACAGTGCCTGTGCCAAGT 1890
    |||||
DB 1876 TTAGTAGCCGCTTTGTGATTCAGATCAACTATCCAGCATCACAGTGCCTGTGCCAAGT 1935
    |||||
QY 1891 AGTCTCACTTTGCTTAAACAGTGGCCCAAGAGACAGATGATGATGCTGTGATTCGG 1950
    |||||
DB 1936 AGTCTCACTTTGCTTAAACAGTGGCCCAAGAGACAGATGATGATGCTGTGATTCGG 1995
    |||||
QY 1951 ATATGCCAAAGAGAGCCCAAGTGTCTTTTAAATGAAAAGTGAAGTTCACAC 2010
    |||||
DB 1996 ATATGCCAAAGAGAGCCCAAGTGTCTTTTAAATGAAAAGTGAAGTTCACAC 2055
    |||||
QY 2011 TTAAA 2015
    |||||
DB 2056 TTAAA 2060
    |||||

RESULT 8
ABNS9917
ID ABNS9917 standard; cDNA; 2010 BP.
XX
AC ABNS9917;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 328.
XX
KW Human; anti-naeemic; vulnery; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wenman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
XX
DR P-PsDB; ABB97504.
XX
PT An isolated polynucleotide for treating diseases associated with its
XX encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Claim 1; SEQ ID NO 328; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention
XX
SQ Sequence 2010 BP; 585 A; 446 C; 527 G; 452 T; 0 U; 0 Other;
    |||||
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Query Match 87.7%; Score 1768; DB 6; Length 2010;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 47 CAGGCCAGCATCTCTCAGAAAAAGCATCCCGAGAGGAAAGCAATCGTTAAACATCTT 106
Db 243 CAGGGCAGCATCTCTCAGAAAAAGCATCCCGAGAGGAAAGCAATCGTTAAACATCTT 302
QY 107 AGGTGAGCTCTAGCCCTCTCGGAATTTGCTCTCTCAGTGGAAACCCCGAAGACTGATC 166
Db 303 AGGTGAGCTCTAGCCCTCTCGGAATTTGCTCTCTCAGTGGAAACCCCGAAGACTGATC 362
QY 167 AGTCTTCAGTCTTAAACCAATGAGCCAGAGGTTTGATGAGTTCGCGCGAGCTAGCCATAG 226
Db 363 AGTCTTCAGTCTTAAACCAATGAGCCAGAGGTTTGATGAGTTCGCGCGAGCTAGCCATAG 422
QY 227 ACTTTTCTCAGAGAGAGTGGGCTGTCTGAACTCTGCTCAGAGGAACTGTACTGGAGAG 286
Db 423 ACTTTTCTCAGAGAGAGTGGGCTGTCTGAACTCTGCTCAGAGGAACTGTACTGGAGAG 482
QY 287 TGATGCTGAGAACTACAGTAATTGCTGCTCACTGGAATTTGAGTCAGCATATGAAAAA 346
Db 483 TGATGCTGAGAACTACAGTAATTGCTGCTCACTGGAATTTGAGTCAGCATATGAAAAA 542
QY 347 AGAGTTTACCTACAGAAAAAAACATTCATGAATAAGGCTTCCAAAAGAAATTCAGATA 406
Db 543 AGAGTTTACCTACAGAAAAAAACATTCATGAATAAGGCTTCCAAAAGAAATTCAGATA 602
QY 407 GAAAGATTAATTCCTTGGCCGTAACTGGATATGTGAAGATA CGCTTGAAGACCAAGC 466
Db 603 GAAAGATTAATTCCTTGGCCGTAACTGGATATGTGAAGATA CGCTTGAAGACCAAGC 662
QY 467 GCTCCAGAGGAGGATATGTCATTCAGATGATCATCAATTAATGTCAAAAGGCTGTACTA 526
Db 663 GCTCCAGAGGAGGATATGTCATTCAGATGATCATCAATTAATGTCAAAAGGCTGTACTA 722
QY 527 GAGAAGGCAACCCCTCTAGAAACATATCAGACATCATATAAGAGAAATTCCTTGAATGA 586
Db 723 GAGAAGGCAACCCCTCTAGAAACATATCAGACATCATATAAGAGAAATTCCTTGAATGA 782
QY 587 AGGACTGTGGGAAGGCTTTAGTCGTGCTATCAACTTAAGTCAAGATCAGAAATCCATA 646
Db 783 AGGACTGTGGGAAGGCTTTAGTCGTGCTATCAACTTAAGTCAAGATCAGAAATCCATA 842
QY 647 CTGTGTGAGAAACCTTATGTAATGTAAAGAAATGTAAAGAGGCTTCCGTTGGGCAATCAG 706
Db 843 CTGTGTGAGAAACCTTATGTAATGTAAAGAAATGTAAAGAGGCTTCCGTTGGGCAATCAG 902
QY 707 TTAACAACATCAAAAAATTCATACCTGAGGAGAGAGCCCTACAGATGTAAAGACTGGAGA 766
Db 903 TTAACAACATCAAAAAATTCATACCTGAGGAGAGAGCCCTACAGATGTAAAGACTGGAGA 962
QY 767 AGGCTTTTCGATGGGCTCAAGCCTCGTTATTCATTAAGAGATTCATATCTGTGAAAAAC 826
Db 963 AGGCTTTTCGATGGGCTCAAGCCTCGTTATTCATTAAGAGATTCATATCTGTGAAAAAC 1022
QY 827 CCTATGAATGTAAAGACTGTGAAAGGCTTTCGCGGTGTGTATGAGCTCATCAGCAC 886
Db 1023 CCTATGAATGTAAAGACTGTGAAAGGCTTTCGCGGTGTGTATGAGCTCATCAGCAC 1082
QY 887 AGAGATTCACACACTGGGAGAAAGACTACAGATGCAAAAGCTGTGGGAAAGCTTTAGCC 946
Db 1083 AGAGATTCACACACTGGGAGAAAGACTACAGATGCAAAAGCTGTGGGAAAGCTTTAGCC 1142
QY 947 GTGTGTATTAACCTTATTCAGCAAGAGAAATTCATAGTGGGAGAAAGCTTTACAGGTGA 1006
Db 1143 GTGTGTATTAACCTTATTCAGCAAGAGAAATTCATAGTGGGAGAAAGCTTTACAGGTGA 1202
QY 1007 AAGACTGTGGGAAGGCTTTATTTGTGTCAAGCTCATTTAGAGATTAAGAAATTCACA 1066
Db 1203 AAGACTGTGGGAAGGCTTTATTTGTGTCAAGCTCATTTAGAGATTAAGAAATTCACA 1262
QY 1067 CAGGTGAGAAACCTTATGATGTCAAGATGTGGGAAGGCTTTTACTCGAGTCAATTAAC 1126

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Db 1263 CAGGTGAGAAACCTTATGATGTCAAGATGTGGGAAGGCTTTTACTCGAGTCAATTAAC 1322
QY 1127 TTAACAACATCAAGAAATTCACACACCGGTGAGAGCTTCACGAATGTAAAGAGTGGGA 1186
Db 1323 TTAACAACATCAAGAAATTCACACACCGGTGAGAGCTTCACGAATGTAAAGAGTGGGA 1382
QY 1187 AGGCTTTTCGCGGTGTGAGAGCTCGTTAAGCAGAGAGGATACATACGGGCGAAGAC 1246
Db 1383 AGGCTTTTCGCGGTGTGAGAGCTCGTTAAGCAGAGAGGATACATACGGGCGAAGAC 1442
QY 1247 CGTACAGTGCACAGAAATGTGGGAAGGCTTCAATTGTGTGCTATCACTCACTCAGCAG 1306
Db 1443 CGTACAGTGCACAGAAATGTGGGAAGGCTTCAATTGTGTGCTATCACTCACTCAGCAG 1502
QY 1307 AGAGATTCACACACAGGCGAAACCCCGTATTAATGTAAAGAGTGTGGAAAGGCTTTCA 1366
Db 1503 AGAGATTCACACACAGGCGAAACCCCGTATTAATGTAAAGAGTGTGGAAAGGCTTTCA 1562
QY 1367 ATGATTCGAGCCTCGTGAAGCATGAGAGATTCATACCGGGGTGAACCTTATGGGTGA 1426
Db 1563 ATGATTCGAGCCTCGTGAAGCATGAGAGATTCATACCGGGGTGAACCTTATGGGTGA 1622
QY 1427 CAGAAATGTGGGAAGAGCTTTAGTCAAGGCTCATCACTTACACAGATCAGAAAAAGCACA 1486
Db 1623 CAGAAATGTGGGAAGAGCTTTAGTCAAGGCTCATCACTTACACAGATCAGAAAAAGCACA 1682
QY 1487 GTGGGGCGAAATCCTACGAATGTAAAGAGTGGGGAAGGCAATGTAAACCACTTAAACATC 1546
Db 1683 GTGGGGCGAAATCCTACGAATGTAAAGAGTGGGGAAGGCAATGTAAACCACTTAAACATC 1742
QY 1547 TCCGGAACATCAGAGAGATCCACACAGTGAAGAGCCTTTTGAACGCAATGAGCCGCTC 1606
Db 1743 TCCGGAACATCAGAGAGATCCACACAGTGAAGAGCCTTTTGAACGCAATGAGCCGCTC 1802
QY 1607 GTATCTATGTTTCCCTTCCACAGTTTGTATCACTGAGTCACTGCACTTCAAAAAATAT 1666
Db 1803 GTATCTATGTTTCCCTTCCACAGTTTGTATCACTGAGTCACTGCACTTCAAAAAATAT 1862
QY 1667 TAAATGAAAAATTCAGAAATTAAGAAATTTTAAGTCTCAATGTGTGCTTCTGAGTA 1726
Db 1863 TAAATGAAAAATTCAGAAATTAAGAAATTTTAAGTCTCAATGTGTGCTTCTGAGTA 1922
QY 1727 GCGTGTATGAATCTCTGCTGCTGCGGCTCCAGCCGCGCGGGAATGTAGTCACTCCCTTGG 1786
Db 1923 GCGTGTATGAATCTCTGCTGCTGCGGCTCCAGCCGCGCGGGAATGTAGTCACTCCCTTGG 1982
QY 1787 TCCAGCACATCCACGCTGTATACGCCAC 1814
Db 1983 TCCAGCACATCCACGCTGTATACGCCAC 2010

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RESULT 9
AAH9589/c
ID AAH9589 standard; cDNA, 1453 BP.

AAH9589;

16-OCT-2001 (first entry)

Human protein encoding cDNA sequence SEQ ID NO:424.

Human; cancer; HIV infection; human immunodeficiency virus;
antibacterial; antineoplastic; antiarthritic; immunosuppressive;
anti-infective; endocrine; cardiac; central nervous system; virucide;
anti-HIV; fungicide; antimetagen; cardiovascular; anaemia;
antiallergic; haemostatic; antitumor; osteoporosis; eczema;
dermatological; antiallergic; antineoplastic; antidiabetic; cytotoxic;
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
anti-anaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoietic disorder; platelet disorder; asthma;
thrombocytopenia; osteoporosis; severe combined immunodeficiency;

Db 133 CAAGCAGTCCCTGCTTGGCTTAACAGTGCGCCAGAGAGACAGAGNAGTATGATGCTGG 74
QY 1943 TGATTTCGATATGCCAAGAGAGCCACAAAGTGCCTCTTTTAATGAAAAGGTGAAG 2002
Db 73 TGATTTCGATATGCCAAGAGAGCCACAAAGTGCCTCTTTTAATGAAAAGGTGAAG 14
QY 2003 TTCTCACTTAA 2015
Db 13 TTCTCACTTAA 1
RESULT 10
AD13363
ID AD13363 standard; cDNA; 1429 BP.
XX AD13363;
AC AD13363;
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #689.
XX
XX Human; gene; ss; immunological response; immunopathological condition;
KM Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KM irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KM acute monocytic leukemia; antiinflammatory; antiasthmatic; antiulcer;
KM osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Selthamer JJ;
DR WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1, SEQ ID NO 689; 50pp; English.
XX
XX The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or

CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1429 BP; 424 A; 311 C; 360 G; 329 T; 0 U; 5 Other;
Query Match 69.4%; Score 1397.8; DB 11; Length 1429;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1411; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 595 GGGAAAGCCTTTAGTCGTGGCTATCACTTATGTAACATCAGAAAATCCATCTGTGAG 654
Db 10 GGGAAAGCCTTTAGTCGTGGCTATCACTTATGTAACATCAGAAAATCCATCTGTGAG 69
QY 655 AAACCTTATGAATGTAAAGAAATGTAAAGAGCCTTCGTTGGGGCAATCAGTTACTCA 714
Db 70 AAACCTTATGAATGTAAAGAAATGTAAAGAGCCTTCGTTGGGGCAATCAGTTACTCA 129
QY 715 CATCAAAAATTCATACCTGGGGAAGAGCCTTACGAATGTAAAGACTGTGGG 772
Db 130 CATCAAAAATTCATACCTGGGGAAGAGCCTTACGAATGTAAAGACTGTGGGGAAGCCTT 189
QY 773 TTGCATGGGGCTCAAGCCTCGTTATTCTAATGAAGATTCACTGTGTAAGAAACCTTATG 832
Db 190 TTGCATGGGGCTCAAGCCTCGTTATTCTAATGAAGATTCACTGTGTAAGAAACCTTATG 249
QY 833 AATGTAAAGACTGTGAAAGAGCCTTCGCGGTGTATGAGTCACTCAGACAGAGAT 892
Db 250 AATGTAAAGACTGTGAAAGAGCCTTCGCGGTGTATGAGTCACTCAGACAGAGAT 309
QY 893 TTCAACTGGGGGAAGAACTACATACGAATGCAAGAGCTGTGGGAAGCCTTTAGCCGTGT 952
Db 310 TTCAACTGGGGGAAGAAAGNTACGAATGCAAGAGCTGTGGGAAGCCTTTAGCCGTGT 369
QY 953 ATTAACCTTATTCAGACAGAGAAATTCATGATGGGGGAAGCCTTACAGATTAAGAAGCT 1012
Db 370 ATTAACCTTATTCAGACAGAGAAATTCATGATGGGGGAAGCCTTACAGATTAAGAAGCT 429
QY 1013 GTGGGAAGCCTTTATTTGTGGTTCAAGCCTCATTCAGCATTAAGAAATTCACACAGGTG 1072
Db 430 GTGGGAAGCCTTTATTTGTGGTTCAAGCCTCATTCAGCATTAAGAAATTCACACAGGTG 489
QY 1073 AGAAACCTTATGAATGTCAAGAAATGTGGGAAGCCTTTATCTGATCAATTACCTTACTC 1132
Db 490 AGAAACCTTATGAATGTCAAGAAATGTGGGAAGCCTTTATCTGATCAATTACCTTACTC 549
QY 1133 AGCATCAGAAATCCACACCGGTGGAAGCCTCAGCAATGTAAAGAGTGTGGGAAGGCT 1192
Db 550 AGCATCAGAAATCCACACCGGTGGAAGCCTCAGCAATGTAAAGAGTGTGGGAAGGCT 609
QY 1193 TTGCGTGGGGTTGAGCCTCGTTAAGCAGAGAGATCATACGGGCGAGAAGCCGTACA 1252
Db 610 TTGCGTGGGGTTGAGCCTCGTTAAGCAGAGAGATCATACGGGCGAGAAGCCGTACA 669
QY 1253 AGTCACAGAAATGTGGGAAGCCTTCAATTGTGCTATCACTCACTCAGACGAGAGAA 1312
Db 670 AGTCACAGAAATGTGGGAAGCCTTCAATTGTGCTATCACTCACTCAGACGAGAGAA 729
QY 1313 TTCACAGAGGGGAAGCCCGTAAATGTAAAGAGTGTGGGAAGCCTTCAATTATGAT 1372
Db 730 TTCACAGAGGGGAAGCCCGTAAATGTAAAGAGTGTGGGAAGCCTTCAATTATGAT 789
QY 1373 CGAGCCTGTGAACATGAGAAATTCATACCGGGGTGAAGCCCTATGCGGTGTACAGAT 1432
Db 790 CGAGCCTGTGAACATGAGAAATTCATACCGGGGTGAAGCCCTATGCGGTGTACAGAT 849
QY 1433 GTGGGAAGCCTTATGATACGGGCACTCAGCTTACCAATCAGAAAGCACTGTGGG 1492
Db 850 GTGGGAAGCCTTATGATACGGGCACTCAGCTTACCAATCAGAAAGCACTGTGGG 909
QY 1493 CGAAATCTCAAGAAATGTAAAGAGTGTGGGAAGCCTATTAACCACTTAACCATCTCGAG 1552

Db 910 CGAAATCTTACGATGTAAGAGTGGGAGGAGCATGTATACCACTTCCGAG 969
 QY 1553 AACATCAGAGATCCACACAGTTGAAAGCCTTTGAAAGCAGTAGCCCGCTGATCT 1612
 Db 970 AACATCAGAGATCCACACAGTTGAAAGCCTTTGAAAGCAGTAGCCCGCTGATCT 1029
 QY 1613 ATGTTTCGCTTCCACAGTTGTTTACCTGACATCACTGACAGTTCAAAAATTTAAATG 1672
 Db 1030 ATGTTTCGCTTCCACAGTTGTTTACCTGACATCACTGACAGTTCAAAAATTTAAATG 1089
 QY 1673 GAAATTCAGAAATTAAGATTTTAAATGTTTCAATGTTGTCCTTCTGAGTAGGCTGA 1732
 Db 1090 GAAATTCAGAAATTAAGATTTTAAATGTTTCAATGTTGTCCTTCTGAGTAGGCTGA 1149
 QY 1733 TGAATTCCTCGCTGCTCGGCTCCAGCCGCGGAGGATGATCATCCCTTGGTCAGC 1792
 Db 1150 TGAATTCCTCGCTGCTCGGCTCCAGCCGCGGAGGATGATCATCCCTTGGTCAGC 1209
 QY 1793 ACATCCACGCTGTATACGCGCACCCACCTGCTAGTACCTTAGAGCCGCTTGGTATCA 1852
 Db 1210 ACATCCACGCTGTATACGCGCACCCACCTGCTAGTACCTTAGAGCCGCTTGGTATCA 1269
 QY 1853 GATCACTATCCACAGATCAAGTGGCTGTGCCCCAGTAGTCTCTCACTTTGCTTAACAGT 1912
 Db 1270 GATCACTATCCACAGATCAAGTGGCTGTGCCCCAGTAGTCTCTCACTTTGCTTAACAGT 1329
 QY 1913 GGGCCGAGAGAGAGAGTAGTATGCTGGTGAATTCGCAATGCAAGAGAGAGAGAGAG 1972
 Db 1330 GGGCCGAGAGAGAGAGTAGTATGCTGGTGAATTCGCAATGCAAGAGAGAGAGAGAG 1389
 QY 1973 AGTGCTTCTTTTAAATGAAAGGTGAAAGTTCTCAACTT 2012
 Db 1390 AGTGCTTCTTTTAAATGAAAGGTGAAAGTTCTCAACTT 1429

RESULT 11
 ADS83430
 ID ADS83430 standard; cDNA; 1429 BP.
 XX
 AC ADS83430;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Human lymph node cDNA #689.
 XX
 KW ss; gene; human; immunological response; blood cell; cancer;
 KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
 KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
 KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
 XX
 OS Homo sapiens.
 XX
 PN US2004077003-A1.
 XX
 PD 22-APR-2004.
 XX
 PF 14-AUG-2003; 2003US-00641643.
 XX
 PR 09-FEB-1998; 98US-00023655.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Cocke BG, Stuart SG, Seilhamer JJ;
 XX
 DR WPI, 2004-387937/36.
 XX
 PT New compositions having a number of first, second and third
 PT polynucleotide probes, useful in research and diagnostic applications in
 PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
 PT infections.
 XX
 PS Claim 15; SEQ ID NO 689; 16pp; English.

CC The invention relates to polynucleotides which are used as probes to
 CC detect genes differentially expressed in an immunological response,
 CC abundantly expressed in an immunological response and/or coding for a
 CC polypeptide known to regulate blood cell biology. The polynucleotides are
 CC useful in research and diagnostic applications particularly in cancer and
 CC immunopathological conditions, such as AIDS, allergy, anaemia, asthma,
 CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
 CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
 CC present sequence represents a human lymph node cDNA used to detect blood
 CC cell and immunological response gene expression. Note: The present
 CC sequence does not appear in the printed specification but was obtained in
 CC electronic format from the USPTO web site
 CC (seqdata.uspto.gov/sequence.html?docid=20040077003).
 CC XX

SQ Sequence 1429 BP; 424 A; 311 C; 360 G; 329 T; 0 U; 5 Other;

Query Match 69.4%; Score 1397.8; DB 13; Length 1429;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1411; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
 QY 595 GGAAGGCTTATGTCGTCGCTATCACTTATCAATCAGAAATCCATCTGTGTAG 654
 Db 10 GGAAGGCTTATGTCGTCGCTATCACTTATCAATCAGAAATCCATCTGTGTAG 69
 QY 655 AAACCTTATGATGTAAGATGTAAGAAAGCCTTCCTGGGGCAATAGCTTACTCA 714
 Db 70 AAACCTTATGATGTAAGATGTAAGAAAGCCTTCCTGGGGCAATAGCTTACTCA 129
 QY 715 CATCAAAAATTCATCTGGGGGAGAAAGCCTTCGATGTAAGATGTAAGATGTAAG 772
 Db 130 CATCAAAAATTCATCTGGGGGAGAAAGCCTTCGATGTAAGATGTAAGATGTAAG 189
 QY 773 TTCGATGGGGCTCAAGCCTCGTTATTCATTAAGAGATTCATCTGTGTAAGAAACCTTAG 832
 Db 190 TTCGATGGGGCTCAAGCCTCGTTATTCATTAAGAGATTCATCTGTGTAAGAAACCTTAG 249
 QY 833 AATGTAAGATCTGTGAAAGGCTTTTGGCTGTGTAGTACCTCACTGACACAGAGAT 892
 Db 250 AATGTAAGATCTGTGAAAGGCTTTTGGCTGTGTAGTACCTCACTGACACAGAGAT 309
 QY 893 TCCACATGGGGAGAAAGCTACGAAATGCAAGATCTGTGGGAAAGCCTTAGCCGTGT 952
 Db 310 TCCACATGGGGAGAAAGCTACGAAATGCAAGATCTGTGGGAAAGCCTTAGCCGTGT 369
 QY 953 ATTAACCTTATTCAGCAAGAGAAATTCATATGTGGGAGAGCCTTACAGATGTAAGACT 1012
 Db 370 ATTAACCTTATTCAGCAAGAGAAATTCATATGTGGGAGAGCCTTACAGATGTAAGACT 429
 QY 1013 GTGGGAAGGCTTTTATTTGTGTGTTCAAGCCTCATTCAGATTAAGAAATTCACACAGGTG 1072
 Db 430 GTGGGAAGGCTTTTATTTGTGTGTTCAAGCCTCATTCAGATTAAGAAATTCACACAGGTG 489
 QY 1073 AGAAACCTTATGATGTAAGATGTAAGATGTAAGAGCCTTTTCTGAGTCAATTCCTTACTC 1132
 Db 490 AGAAACCTTATGATGTAAGATGTAAGATGTAAGAGCCTTTTCTGAGTCAATTCCTTACTC 549
 QY 1133 AGCATCAGAAAGATCCACACCGGTGAGAGCCTTCACGAATGTAAGAGTGTGGAAAGGCTT 1192
 Db 550 AGCATCAGAAAGATCCACACCGGTGAGAGCCTTCACGAATGTAAGAGTGTGGAAAGGCTT 609
 QY 1193 TTGCTGTGGGTTTGAAGCCTCGTTAAGACGAGAGATCATACGCGCGAGAAAGCCTTACA 1252
 Db 610 TTGCTGTGGGTTTGAAGCCTCGTTAAGACGAGAGATCATACGCGCGAGAAAGCCTTACA 669
 QY 1253 AGTGCAAGAAATGTGGAAAGGCTTCAATTTGTGCTATCACTCACTCAGCAGAGAA 1312
 Db 670 AGTGCAAGAAATGTGGAAAGGCTTCAATTTGTGCTATCACTCACTCAGCAGAGAA 729
 QY 1313 TCCACACAGGCGAAACCCGCTATTAATGTAAGAGTGTGGAAAGGCTTCACTTATGAT 1372
 Db 730 TCCACACAGGCGAAACCCGCTATTAATGTAAGAGTGTGGAAAGGCTTCACTTATGAT 789
 QY 1373 CGAGCTCGTGAACAATGAGAAATTCATACCGGGGTGAAGCCTTATGGGTGTAAGAAAT 1432

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Db 790 CGAGCTCGTGAACATGAGAAATTCATCCGGGGTGAACCTATGGGTATACAGAT 849
Qy 1433 GTGGGAAGAGCTTTAGTCA CGGCCATCAGCTTACCAACATCAGAAAAAGCA CAGTGGG 1492
Db 850 GTGGGAAGAGCTTTAGTCA CGGCCATCAGCTTACCAACATCAGAAAAAGCA CAGTGGG 909
Qy 1493 CGAAATCTCAAGATGTAAGAGGTGCGGGAAGGCATGTATACCACTTAAACATCTCCAG 1552
Db 910 CGAAATCTCAAGATGTAAGAGGTGCGGGAAGGCATGTATACCACTTAAACATCTCCAG 969
Qy 1553 AACATCAGAGATCCACAAGAGTGAAGAGCTTTTGAAGAGAGTGAAGAGAGTGAAGT 1612
Db 970 AACATCAGAGATCCACAAGAGTGAAGAGCTTTTGAAGAGAGTGAAGAGAGTGAAGT 1029
Qy 1613 ATGTTTGGCTTCCACAGATTTGTATCCTGACATCACTGACAGTTCAAAAATATTAATG 1672
Db 1030 ATGTTTGGCTTCCACAGATTTGTATCCTGACATCACTGACAGTTCAAAAATATTAATG 1089
Qy 1673 GAAATTTCCAGAAATTAAGAAATTTTAAGTCTCAATGGTGGCTTTGAGTAGCGTGA 1732
Db 1090 GAAATTTCCAGAAATTAAGAAATTTTAAGTCTCAATGGTGGCTTTGAGTAGCGTGA 1149
Qy 1733 TGAATCTCGCTGCTCGGCTCCAGCGGGCGGGGATGTAGTCACTCCCTTGGTCCAGC 1792
Db 1150 TGAATCTCGCTGCTCGGCTCCAGCGGGCGGGGATGTAGTCACTCCCTTGGTCCAGC 1209
Qy 1793 ACATCCAGCTGTATACGCCACCAACCTCTGATAGTACTTAAAGCCGTCTTGGTATCA 1852
Db 1210 ACATCCAGCTGTATACGCCACCAACCTCTGATAGTACTTAAAGCCGTCTTGGTATCA 1269
Qy 1853 GATCAACTATCCAGATCA CAGTGCCTGTGCCAAAGTACTCACTTTGCTTAAACAGT 1912
Db 1270 GATCAACTATCCAGATCA CAGTGCCTGTGCCAAAGTACTCACTTTGCTTAAACAGT 1329
Qy 1913 GGGCCCAAGAGAGAGAGTGAAGTCTGTGATTCGATATGCCAAAGAGAGAGAGAGAG 1972
Db 1330 GGGCCCAAGAGAGAGAGTGAAGTCTGTGATTCGATATGCCAAAGAGAGAGAGAGAG 1389
Qy 1973 AGTGTCTCTTTTAAATGAAAAGTGAAGTCTCAACTT 2012
Db 1390 AGTGTCTCTTTTAAATGAAAAGTGAAGTCTCAACTT 1429

RESULT 12
ADFI4367
ID ADFI4367 standard; DNA; 4483 BP.
XX
AC ADFI4367;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human endometrial-specific DNA - SEQ ID 332.
XX
KW endometrial-specific; ESNAs; ESP; vaccine; cancer;
KW squamous cell carcinoma; endometrium; gene therapy; transgenic; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2003059927-A1.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041413.
XX
PR 21-DEC-2001; 2001US-0342751P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Liu C;
XX
DR WPI; 2003-598500/56.
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XX New endometrial specific genes and proteins, useful in gene therapy or as
PT vaccines for treating endometrial cancer or non-cancerous endometrial
PT diseases, as well as for diagnosing, monitoring or staging such diseases.
PS Claim 1; SEQ ID NO 332; 1156bp; English.
XX
CC The invention relates to a novel isolated endometrial specific nucleic
CC acid molecule (ESNA) comprising a sequence that encodes an endometrial-
CC specific polypeptide (ESP). The molecules of the invention may be useful
CC for generating a vaccine and for identifying, diagnosing, monitoring,
CC staging, imaging and treating endometrial cancer, such as squamous cell
CC carcinoma, as well as non-cancerous disease states in the endometrium.
CC Furthermore, the polypeptides and polynucleotides may be useful in gene
CC therapy, production of transgenic animals and cells and in the production
CC of engineered endometrial tissue for treatment and research. The current
CC sequence is that of the human endometrial-specific DNA of the invention.
XX
SQ Sequence 4483 BP; 1262 A; 960 C; 1086 G; 1166 T; 0 U; 9 Other;

Query Match 36.5%; Score 734.6; DB 10; Length 4483;
Best Local Similarity 91.2%; Pred. No. 1.9e-221;
Matches 791; Conservative 0; Mismatches 74; Indels 2; Gaps 1;

Qy 47 CAGGCGAGATCCTCAGAAAAAGCATCCCGAGAGAGAGAGAGATCGTTAAACATCTT 106
Db 1184 CAGGCGAGATCCTCAGAAAAAGCATCCCGAGAGAGAGAGAGATCGTTAAACATCTT 1243
Qy 107 AGGTGAGCTTACCTCTCGAATTTGTTCTTTCAGTGAAGAACCCGAGAAAGTATC 166
Db 1244 AGGTGAGCTTACCTCTCGAATTTGTTCTTTCAGTGAAGAACCCGAGAAAGTATC 1303
Qy 167 AGTCTTCAAGTTTAAACATATGCGCCAGGTTTGGTGAAGTTCGCCGATAGCATAG 226
Db 1304 AGTCTTCAAGTTTAAACATATGCGCCAGGTTTGGTGAAGTTCGCCGATAGCATAG 1363
Qy 227 ACTTTTTCAGAGAGAGAGGCGCTGTGAATCTGCTCAGAGAGAGAGCTGTGCGGAGG 286
Db 1364 ACTTTTTCAGAGAGAGAGGCGCTGTGAATCTGCTCAGAGAGAGAGCTGTGCGGAGG 1423
Qy 287 TGATGCTGAGAGACTACAGTATCTGTCTCACTGATTTGGAGTCAAGATATGAATAA 346
Db 1424 TGATGCTGAGAGACTACAGTATCTGTCTCACTGATTTGGAGTCAAGATATGAATAA 1483
Qy 347 AGAGTTTACCTACAGAAAAAAACATTCAATGAATAAAGGCTTCAAAAGAAATTCAGTA 406
Db 1484 AGAGTTTACCTACAGAAAAAAACATTCAATGAATAAAGGCTTCAAAAGAAATTCAGTA 1543
Qy 407 GAAAGAGTAAATCCCTTGGCGCTAATGGAATGGAAGTACGCTTGAAGACCAACAGC 466
Db 1544 GAAAGAGTAAATCCCTTGGCGCTAATGGAATGGAAGTACGCTTGAAGACCAACAGC 1603
Qy 467 GCTCCAGAGAGAGATGATCAATCAGATGATCATATATATCAAAAGGCTGTACTATA 526
Db 1604 GCTCCAGAGAGAGATGATGATCAATCAGATGATCATATATATCAAAAGGCTGTACTATA 1663
Qy 527 GAGAAAGCAACCCCTCTTAAGACATCAGAGATCATATGAAGAAATTCCTTTGAATGTA 586
Db 1664 GAGAAAGCAACCCCTCTTAAGACATCAGAGATCATATGAAGAAATTCCTTTGAATGTA 1723
Qy 587 AGGACTGTGGGAAGGCTTTAATCGTGGCTATCACTTAAGTAAATCAGAAATTCATTA 646
Db 1724 AGGACTGTGGGAAGGCTTTAATCGTGGCTATCACTTAAGTAAATCAGAAATTCATTA 1783
Qy 647 CTGTGAGAAACCTTATGATGTAAGAAATGTAAGAGGCTTCCGTTGGGGCAATCAGC 706
Db 1784 CTGTGAGAAACCTTATGATGTAAGAAATGTAAGAGGCTTCCGTTGGGGCAATCAGC 1843
Qy 707 TTACTCAACATCAAAAATTTACTGCGGAGAGAGCCCTTCAAGATGTAAGAGTGGGA 766
Db 1844 TTACTCAACATCAAAAATTTACTGCGGAGAGAGCCCTTCAAGATGTAAGAGTGGGA 1901
Qy 767 AGGCTTTTGTGATGGGGCTCAAGCTCGTATTCATTAAGAGATTCATCTGATGAAGAAC 826
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Db      1902 AGAGCTTTGTCACGCCCATCAGCTTACACAAACATCAGAAAACGACAGTGGGCGCAAAAT 1961
Qy      827 CCTATGAATGTAAAGACTGTGGAAGCCCTTTGCGGTGTGTATGCTTCACTCAGACAC 886
Db      1962 CCTAGCAATGTATGAGTGCAGGAGGCAATGTAAACCACTTCCTCGAAGAACATC 2021
Qy      887 AGAGATTCCACACTGGGAGAGAAAGACT 913
Db      2022 AGAGATCCACACAGTGAAGAGCCT 2048

RESULT 13
ABA92946
ID      ABA92946 standard; cDNA; 2143 BP.
XX
XX      ABA92946;
XX
XX      09-APR-2002 (first entry)
XX
XX      Human cartilage zinc finger protein CZF-2 encoding cDNA SEQ ID NO:3.
XX
XX      Human; cartilage zinc finger; CZF-1; CZF-2; chromosome 19; 19q13.4;
XX      chondrogenesis; fracture callus; tumour; chondrocyte; gene; se.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      25..1581
XX              /tag=a
XX              /product="CZF-2"
XX              /note="cartilage zinc finger protein"
XX
XX      MO200195860-A2.
XX
XX      20-DEC-2001.
XX
XX      14-JUN-2001; 2001WO-US019108.
XX
XX      14-JUN-2000; 2000US-0211384P.
XX
XX      (UYCA-) UNIT CASE WESTERN RESERVE.
XX
XX      Hering TM, Johnstone B;
XX
XX      WPI; 2002-090168/12.
XX      P-PDB; ABB05388.
XX
XX      Detecting and staging chondrogenesis in cells, comprises using novel
XX      markers which are isolated polynucleotides referred as cartilage zinc
XX      finger-1 and 2 or antibodies specific for the proteins encoded by CZF-1
XX      and CZF-2.
XX
XX      Claim 14; Fig 5; 69p; English.
XX
XX      The present invention describes a method for determining the extent of
XX      chondrogenesis in a cell and the presence of cells with characteristics
XX      of chondrocytes in a tissue sample obtained from a tumour or fracture
XX      callus. The method comprises using novel markers, which are isolated
XX      polynucleotides referred as cartilage zinc finger-1 (CZF-1) and CZF-2 or
XX      their fragments, or antibodies specific for the proteins encoded by CZF-1
XX      and CZF-2. CZF-1 and CZF-2 proteins are useful for preparing antibodies
XX      which are useful as research tools for identifying tissues that contain
XX      normal or elevated levels of the protein, for purifying the protein, for
XX      identifying and diagnosing diseases associated with elevated or reduced
XX      levels of CZF proteins, monitoring the effect of therapeutic agents on
XX      the synthesis of CZF proteins and for identifying other proteins,
XX      activators and inhibitors which bind to CZF proteins. Polynucleotides (1)
XX      encoding CZF-1 and CZF-2 can be used as probes to hybridise directly to
XX      cells or tissues suspected of containing chondrocytes, for isolating and
XX      identifying cDNA clones and genomic clones encoding CZF-1 or CZF-2
XX      protein or its allelic forms and as primers to amplify transcripts of
XX      genes which encode the proteins. (1) can also be used as chromosome

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CC      markers to map linked gene positions, to identify chromosomal aberrations
CC      such as translocations, inversions and trisomies and to compare with
CC      endogenous DNA sequences in patients to identify potential genetic
CC      disorders. CZF proteins have been localised to chromosome 19q13.4. The
CC      present sequence encodes human CZF-2 from the present invention
XX
XX      SQ      Sequence 2143 BP; 735 A; 331 C; 478 G; 599 T; 0 U; 0 Other;
XX
XX      Query Match      34.9%; Score 703; DB 6; Length 2143;
XX      Best Local Similarity 69.7%; Pred. No.1.3e-211;
XX      Matches 1006; Conservative 0; Mismatches 410; Indels 27; Gaps 3;
XX
Qy      172 TTCAGTCTTMAAACATATGCCCCAGGTTTGTGACGTTGCGCAGCTACCAATGACTTT 231
Db      10 TCGAATTCAGAACCATATGCTATGATGGGTGTGTGACATTCAGAGGATGTGCGCATTC 69
Qy      232 TCTCAGAGAGATGGGCGCTGTCTGAACCTGCTCAGAGGAGACTGTATCTGGAGACGTGATG 291
Db      70 TCTCAGAGAGATGGGAGATGCTTGACCTGTCTCAGAGGAGACTGTATCTGTGATGTAAATG 129
Qy      292 CTGAGAACTACAGTACTTGGTCTCACTGATTTGAGATC--AGCATATGAAAATAAG 348
Db      130 TTGAGAACTATATGTAATCTGTGTCTGATCTGATTTGAGATCATAAAACGTAAGACCAA 189
Qy      349 AGTTTACCTACAGAAAAAATCATATGAAATGAGGCTTCCAAAAGAAATTCAGATGA 408
Db      190 AAAATATTTTCAGAAAATGATATTTTGAATTAATTTTCCAGTGGAGATGAAGAC 249
Qy      409 AGAAGTAAATCCCTTGCC-----GTAATCTGATATGTGAAGT 447
Db      250 AAAAGTAAACCTTGCCCTTGAGGATCATCTTCAGAAATTAATTTGAAATGCAAAAC 309
Qy      448 AGCTTGAAGAAGCCAGCGCTCCAGAGGAGATATGTAATCATATGATCATATTAAT 507
Db      310 ATATTGAGGACTAATAAGACATCAAGAGGATCTTATGTAATGATATCACTAT 369
Qy      508 GTCAAAAGGCTGCTACTAGAGAGGACCCCTCTAGAACATCAGACAGA---CATCAT 564
Db      370 GAAAAAATCCTTCTTACAGAAAATGTAATCTTACTACACATCAAAAGAAATTCATTAAT 429
Qy      565 AAGAGAAATTCCTTGAATGTAAAGACTGTGGAGAGCCCTTATAGTGGCTATCAACTT 624
Db      430 ACAGAGAAATCCTATTTGTGAAGATGTGGAGAGCTTGACGTATGCTCAAAACTT 489
Qy      625 AGTCAACATCAGAAATTCATCTGCTGAGAAAACCTTATGAATGTAAAGATTAAGAG 684
Db      490 GTTCAACATGAGAACTCATACAGCTGAAAGCACTTGAATGTAAAGATGTGGAGAG 549
Qy      685 GCCTTCCGTTGGGCAATGAGCTTACTCAACATCAAAAAATTCATATCTGGAGAGAGCC 744
Db      550 AATTATTTAAGTCCATATCAATCATATGATCAGAGATTCATCTGGTGAAGAACCC 609
Qy      745 TACGAATGTAAAGCTGTGGAGAGGCTTTTCATGGGGCTCAAGCCTCGTATTCATTAAG 804
Db      610 TATGAGTGAAGAAATGTGGAGAGACCTTAAAGCTGGAGATCAAGCCTGTGTTAAACATGAG 669
Qy      805 AGGATTCATATCTGTGTAAGAAAACCTTATGAATGTAAAGACTGTGAAAGGCTTTGCGCGT 864
Db      670 AGAATTCACCTGTGTGAAGAACCTTATGAATGTAAAGATGTGGAGAGGCTTTATGCTGT 729
Qy      865 GGTGATGAGTCACTCAGACACAGATTCACACTGTGGAGAGAAAGATACGAATGCAAA 924
Db      730 GGTATACCTTACCAACATCAGAAAATTCATATTTGGTGTGAATCTTATTAATGTAAAG 789
Qy      925 GACTGTGGAGAGCTTTTACCGCTGTGTATTAATCTTATCAGACAAAGAAATTCATAGT 984
Db      790 GAATGTGGAGAGGCTTTTGTGGGCTCAAGCCTTGCATTAAGATGAGAAATTCATCA 849
Qy      985 GGGGAGAGGCTTACAGATGTAAAGACTGTGGAGAGGCTTTTATTTGTGTTCAAGGCTC 1044
Db      850 GGTGAGAAACCTTATTAATGTAAAGATGTGGAGAGGCTTCAAGTGTGCTATCAACTT 909
Qy      1045 ATTACAGATTAAGAAATTCACACAGGTGAAGAAACCTTATGAATGTCAAGAAATGTGGAGAG 1104

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Db 910 ACTGAGCAGCAAGAAATCATCTGTTAGAGAAACCTTATGATGTAATATATGGAAG 969
Qy 1105 GCCTTACTGAGTCAATTAACCTTAAGCATCAGAGATCCACCGGTGAGAAAGCT 1164
Db 970 GCTTTTGTGGGGCTATCACTTACTGACATCAGATATTTTCAATCTGTGAGAAACCC 1029
Qy 1165 CACGATGTAAAGAGTGGGAAAGCCTTCCGTGGGTTCAGAGCTCTTAAAGACGAG 1224
Db 1030 TATGATGCAAGGAATGTGGGAAGGCTTTTAAATGTGGATCAAGCTTTTAAACATGAA 1089
Qy 1225 AGGATATACATACGGGCGAGAGCCGTACAGATGTCAGATGTGGAAAGCCTTCAATTGT 1284
Db 1090 AGAATTCATCTGCTGAGAGAAACCTTATGATGTAAGATGTGGAAAGCCTTTAGTCT 1149
Qy 1285 GGCATCACTCTCAGCAGCAGAGATCCACAGCGGAAACCCGTATTAATGTAAAG 1344
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Db 1210 GATGTGGGAAGGCTTTAGTTGGGGTTCAGACCTTGTAAACATGAGAGAGTTCACT 1269
Qy 1405 GGGGTGAAACCTTATGGGTGTACAGATGTGGGAAGGCTTTAGTCAAGCCATCAGCTT 1464
Db 1270 GGTGGAAGATCCCATGATGTAAAGATTCGGAAGAACTTTTGTATGTGGTATCACTT 1329
Qy 1465 ACACAATCATGAGAAACGACAGTGGGGGAAATCCTTACGAATGTAAAGAGTGGGGAAG 1524
Db 1330 ACTGACATCAGGTATTTTACACTGTGTGAGAAACCTTATGAATGTAAAGAAATGTGGGAAG 1389
Qy 1525 GCATGTACCACTTAACCATCTCCGAGAACTCAGAGATCCACACATGTAAGAGCC 1584
Db 1390 GCTTTTAAATGTGTGATCAAGCCTTGTCAACATGAAAGATCCATACAGGGGAGAAACCC 1449
Qy 1585 TTT 1587
Db 1450 TAT 1452

```

RESULT 14
ACA62107
ID ACA62107 standard; cDNA; 2143 BP.

AC ACA62107;

DT 20-AUG-2003 (first entry)

DE cDNA encoding human cartilage zinc finger-2 (CZF-2).

XX Human; cartilage zinc finger-2; CZF-1; CZF-2; chondrogenesis; fracture;
KW tumour; chondrosarcoma; bone formation; chondrogenesis detection;
XX chondrogenesis staging; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 25.1581
FT CDS /tag= a
FT /product= "CZF-2"
FT /note= "Cartilage zinc finger-2"

XX US2003039966-A1.

XX 27-FEB-2003.

XX 14-JUN-2001; 2001US-00881578.

XX 14-JUN-2001; 2001US-00881578.

XX (HERI/) HERING T M.
XX (JOHN/) JOHNSTONE B.

PI Hering TM, Johnstone B;
XX WPI: 2003-492160/46.
DR P-PSDB; AB010395.
XX
XX
PT Novel isolated CZF-1 or CZF-2 protein or its variants, useful as an
PT immunogen for preparing an antibody which is immunoreactive with the
PT protein.
XX
XX
XX Claim 12; Fig 5A-C; 35pp; English.

CC The invention describes an isolated CZF-1 or CZF-2 protein (I) or its
CC variants. The polynucleotide (II) encoding (I) or an anti-(I)-antibody
CC are useful for determining the extent of chondrogenesis in a cell or for
CC ascertaining the presence of cells having characteristics of
CC chondrocytes, in a tissue sample obtained from a tissue or fracture
CC cells, by contacting the cell or tissue sample, or RNA isolated from the
CC cell or tissue sample with a nucleic acid probe. (II) is useful for
CC detecting and staging chondrogenesis in cells, for detecting and
CC characterising cells obtained from a tumour that is suspected of being a
CC chondrosarcoma or cells that have characteristics of chondrocytes that
CC may be present in a tumour tissue, to amplify or probe RNA obtained from
CC mesenchymal cells that are being used as screening tools for compounds
CC that are designed to accelerate or retard chondrogenesis, to probe cells
CC obtained from any area of the body where chondrogenesis is suspected of
CC taking place e.g. an area in the body where new bone formation is taking
CC place after a fracture, and to identify chromosomal aberrations to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. An anti-(I)-antibody is useful as for identifying
CC tissues that contain normal or elevated levels of (I) and for purifying
CC (I) by affinity chromatography, for identifying and diagnosing diseases
CC associated with elevated or reduced levels of (I), for monitoring the
CC effect of therapeutic agents on the synthesis of (I) by cells in vitro
CC and in vivo and for identifying other proteins, activators and inhibitors
CC which bind to (I). This sequence encodes human cartilage zinc finger-2
CC (CZF-2), a marker for detecting and staging chondrogenesis

XX Sequence 2143 BP; 735 A; 331 C; 478 G; 599 T; 0 U; 0 Other;

XX Query Match 34.9%; Score 703; DB 8; Length 2143;

XX Best Local Similarity 69.7%; Pred. 1.3e-211;

XX Matches 1006; Conservative 0; Mismatches 410; Indels 27; Gaps 3;

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Qy 232 TCTCAGAGAGAGTGGGCGCTGCTGAACCTGTGAGAGGACCTGTACTGGGACGTGATG 291
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Qy 292 CTGAGAACTACAGTACTGTCTCACTGTGATTTGAGTGC---AGCATATGAAATTAAG 348
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Qy 349 AGTTTACTACAGAAAAAAACATTCATGAATTAAGGCTTCCAAAAGAAATTCAGATTGA 408
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Oy      685 GCCTTCGTTGGGGCAATCAGCTTACTCAACATCAAAAAATTCATACCTGGGAGAACCC 744
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Oy      1105 GCCTTACCTGAGTCAATTACTTACTCAGCATCAGAAAGTCCACACCGGTGAGAGCCT 1164
Db      970 GCTTTTGTGGGGCTATCAACTTACTCAGCATCAGATATTTATATCTGTGTGAGAAACC 1029
Oy      1165 CAGCAATGTAAAGAGTGTGGAGAGGCTTTCGCTGGGGTTCGAGCCTCGTTAAGCAGAG 1224
Db      1030 TATGATGCAAGGAATGTGGAGAGGCTTTTATTTGGGATCAAGTCTTATTCACATGAA 1089
Oy      1225 AGGATACATACGGGGAGAGAGCCGTACAGTGCACAGATGTGGAGAGGCTTCAATTGT 1284
Db      1090 AGAATTCATACCTGTGAGAAACCTTATGATGTAAAGATGTGAGAGGCTTTAGTCGT 1149
Oy      1285 GGCTACACCTCCTCAGACGAGAGAAATCCACAGAGGCGAAACCCCGTTAATGTAAG 1344
Db      1150 GGCTATCACCTTCTCAACATCAGAAATCCTATCTGTGTGAGAAACCTTTGATGTAA 1209
Oy      1345 GAGTGTGGAGAGGCTTTCATTTATGATCGAGCCTCGTGAACATGAGAGATTCATACC 1404
Db      1210 GAATGTGGAGAGGCTTTAGTTGGGTTCAAGCCTTTTAAACATGAGAGATTCATACC 1269
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Oy      1585 TTT 1587
Db      1450 TAT 1452

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RESULT 15
ADC30401

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ID      ADC30401 standard; cDNA, 2832 BP.
XX
AC      ADC30401;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human novel cDNA sequence, SEQ ID NO:483.
XX
KW      Human; diagnostic; drug screening; forensics; gene mapping;
KW      biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW      neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW      ulcers; osteoporosis; autoimmune disease; cancer;
KW      molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW      neuroprotective; antianaemic; anticoagulant; thrombolytic; vlnetary;
KW      anticancer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW      gene therapy; chromosome 19; gene; ss.
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OS      Homo sapiens.
XX
PN      WO2003029271-A2.
XX
PD      10-APR-2003.
XX
PF      24-SEP-2002; 2002WO-US030474.
XX
PR      24-SEP-2001; 2001US-0324631P.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI      Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI      Haley-Vicente D, Dramnac RT;
XX
DR      MPI; 2003-371981/35.
XX
PT      P-Psdb; ADC31372.
XX
PT      New polynucleotide and polypeptide useful for diagnosing, preventing or
PT      treating conditions such as neurodegenerative diseases, anemias, platelet
PT      disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT      cancer.
XX
PS      Claim 1, SEQ ID NO 483; 1185bp; English.
XX
CC      The invention relates to 971 novel human cDNA sequences (ADC39919-
CC      ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC      invention also relates to nucleic acid sequences over 99% identical with
CC      the novel human cDNAs. The invention additionally encompasses expression
CC      vectors and host cells comprising a nucleic acid of the invention; the
CC      recombinant production of a polypeptide of the invention; an antibody
CC      against a polypeptide of the invention; a method of detecting
CC      polynucleotides or polypeptides of the invention; and methods of
CC      identifying a compound which binds to a polypeptide of the invention. The
CC      invention further discloses methods of preventing, treating or
CC      ameliorating a medical condition; kits comprising polynucleotide probes
CC      and/or monoclonal antibodies for carrying out the methods of the
CC      invention; method for the identification of compounds that modulate the
CC      expression or activity of the polynucleotide and/or polypeptide; and 767
CC      contig sequences corresponding to the cDNA sequences of the invention
CC      (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC      -ADC33394). The nucleic acids and polypeptides of the invention are
CC      useful in diagnostics, drug screening, forensics, gene mapping, in the
CC      identification of mutations responsible for genetic disorders or other
CC      traits, for assessing biodiversity, and in producing many other types of
CC      data and products dependent on DNA and amino acid sequences. They are
CC      also used for treating diseases such as Parkinson's disease, Alzheimer's
CC      disease and other neurodegenerative diseases, anaemia, platelet
CC      disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC      cancer. The nucleic acids may also be used as hybridisation probes or
CC      primers, and in the recombinant production of a protein. The polypeptides
CC      are also useful in generating antibodies, as molecular weight markers,
CC      and as food supplements. The present sequence represents a specifically
CC      claimed human cDNA sequence of the invention. Note: The sequence data for
CC      this patent did not form part of the printed specification, but was

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GenCore version 5.1.7
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1958	97.2	2169	6	CO783329 Sequence
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9	1690.8	83.9	138579	8	AC011487 Homo sapi
10	1659.4	82.4	1904	8	AF251515 Homo sapi
11	1645.4	81.7	2838	8	AK128736 Homo sapi
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14	1469.6	72.9	219392	8	AC146884 Callithr
15	1408.8	69.9	1420	6	CQ718116 Sequence
16	1397.8	69.4	1420	6	AR380144 Sequence
17	1091.8	54.2	2148	4	AY375188 Canis fam
18	1063.4	52.8	1084	8	BC009365 Homo sapi

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ALIGNMENTS

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DEFINITION AX113689
ACCESSION AX113689
VERSION AX113689.1 GI:13939857
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Bulterdiek, J., Rippe, V., Weiboom, M. and Belge, G.
Nucleic acid sequences of hyperplasia and tumours of the thyroid
JOURNAL Patent: WO 0127265-A 3 19-APR-2001;
Universitaet Bremen (DE)

FEATURES

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/note="unamed protein product, RITA"

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CKECKKAFRWENQLOHOKHITGKPYECKDCGKAFRWGSLVHKRIHTEKPYECK
DCGKAFRWGDELTOHOKHITGKPYECKDCGKAFRWGSLVHKRIHTEKPYECK
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LNRHREHORHINS"

ORIGIN

Query Match 100.0%; Score 2015; DB 6; Length 2015;
Best local similarity 100.0%; Pred. No. 0;
Matches 2015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1141 AAGATCCACACCGGTGAAGAGCTTCAAGATGTAAAGAGTGTGGAGAGGCTTTTGCTGG 1200
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DEFINITION AF272148
ACCESSION AF272148.1 GI:8575774
VERSION
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2015)
AUTHORS Rippe,V., Belge,G., Meiboom,M., Kazmierczak,B., Fueco,A. and
Bullerdick,J.
TITLE A KRAB zinc finger protein gene is the potential target of 19q13
translocation in benign thyroid tumors
JOURNAL Genes Chromosomes Cancer 26 (3), 229-236 (1999)
PUBMED 10502321
2 (bases 1 to 2015)
AUTHORS Rippe,V., Meiboom,M. and Bullerdick,J.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2000) Center for Human Genetics and Genetic
Counseling, University of Bremen, Loebener Strasse 2, Bremen 28359,
Germany

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RESULT 3
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LOCUS AX427523
DEFINITION Sequence 33 from Patent WO0121836.
ACCESSION AX427523
VERSION AX427523.1 GI:21537669
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
AUTHORS Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
            Bratcher,Shawn,R., Dufour,G.F., Cohen,H.D., Rosen,B.H., Shah,P.,
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            Panzer,S.R., Roseberry,A.M., Wright,R.J., Chen,W., Liu,T.,
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TITLE Molecules for diagnostics and therapeutics
JOURNAL Patent: WO 0121836-A 33 29-MAR-2001;
            Incyte Genomics, Inc. (US)

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AX274843 2173 bp DNA linear PAT 29-OCT-2001
LOCUS Sequence 108 from Patent WO01/2777.
DEFINITION
ACCESSION AX274843
VERSION AX274843.1 GI:16547475
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
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Hillman, J.L., Baughn, M.R., Yue, H., Lal, P., Lu, D.A., Patterson, C.,
Azimzai, Y., Bandman, O., Tang, Y.T., Mathur, P., Shah, P., Au-Young, J.,
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TITLE
Transcription factors
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Patent: WO 01/2777-A 108 04-OCT-2001;
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ACCESSION BD127591
VERSION BD127591.1 GI:23222536
KEYWORDS JP 2002017375-A/3022.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Homindae; Homo.
1 (bases 1 to 2169)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3022-22-JAN-2002;
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PN JP 2002017375-A/3022
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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PI TETSUO OTSUKI, HISASHI KOGA
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 VERSION CQ783329.1 GI:45503259
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 Homidae; Homo.
 REFERENCE
 1 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
 Koga, H.
 Primers for synthesizing full length cDNA clones and their use
 Patent: JP 1396543-A 3469 10-MAR-2004;
 Research Association for Biotechnology (JP)

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Query Match 97.2%; Score 1958; DB 6; Length 2169;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 Query Match 97.2%; Score 1958; DB 6; Length 2169;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1961; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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AUTHORS Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Nimomiyu, K.
TITLE NEBO human cDNA sequencing project
JOURNAL Unpublished
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AUTHORS Isogai, T. and Otsuki, T.
TITLE Direct Submision
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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            Direct Submission
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            3 (bases 1 to 138579)
            DOE Joint Genome Institute and Stanford Human Genome Center.
            Direct Submission
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            Drive, Walnut Creek, CA 94598, USA
            On Feb 28, 2001 this sequence version replaced gi:7690126.
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            www.jgi.doe.gov
            www.shgc.stanford.edu
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ACCESSION AF251515
VERSION AF251515.2 GI:10048469
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REFERENCE
AUTHORS Wu, H., Zhang, S., Qiu, W., Zhang, G., Xia, O., Xiao, C., Huang, X., Huang, M., Agen, F., Fan, T., Yang, J. and Milunsky, A.
TITLE Isolation, characterization, and mapping of a novel human KRAB zinc finger protein encoding gene ZNF463
JOURNAL Biochim. Biophys. Acta 1518 (1-2), 190-193 (2001)
PUBMED 11267678
REFERENCE
AUTHORS Wu, H., Qiu, W., Zhang, S., Zhang, G. and Xiao, C.
TITLE Cloning of azoospermia-related genes
JOURNAL Unpublished
REFERENCE
AUTHORS Wu, H., Qiu, W., Zhang, S., Zhang, G. and Xiao, C.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Medical Genetics, West China University of Medical Sciences, Remiminnanlu 3duan 17, Chengdu, Sichuan 610041, China
REFERENCE
AUTHORS Wu, H., Qiu, W., Zhang, S., Zhang, G. and Xiao, C.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2000) Medical Genetics, West China University of Medical Sciences, Remiminnanlu 3duan 17, Chengdu, Sichuan 610041, China
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QY	1487	GTGGGGGAAATTCCTACGAATGTAAAGAGTGGCGGAGGCAATGTAAACCACTTAAACATC	1546
DB	1677	GTGGGGGAAATTCCTACGAATGTAAAGAGTGGCGGAGGCAATGTAAACCACTTAAACATC	1736
QY	1547	TCCGAGAACATCAGAGATCCACACAGTTGAAGAGCTTTTGAACGAGTAGCCGCTC	1606
DB	1737	TCCGAGAACATCAGAGATCCACACAGTTGAAGAGCTTTTGAACGAGTAGCCGCTC	1796
QY	1607	GTAATGATGTTTGGCTTTCCACAGTTTGTATCTGCACTCACTGCACTGCAAGTCAAAATAT	1666
DB	1797	GTAATGATGTTTGGCTTTCCACAGTTTGTATCTGCACTCACTGCACTGCAAGTCAAAATAT	1856
QY	1667	TAAATGAGAAATTCAGAGAAATTAAGAAATTTTAAGTCTAAA 1707	
DB	1857	TAAATGAGAAATTCAGAGAAATTAAGAAATTTTAAGTCTAAA 1897	

RESULT 11
 AK128736 2838 bp mRNA linear PRI 30-JAN-2004
 LOCUS AK128736
 DEFINITION Homo sapiens cDNA FLJ16775 fis, clone BRCAN202100, highly similar
 to Homo sapiens zinc finger protein 463 (ZNF463).
 ACCESSION AK128736
 VERSION AK128736.1 GI:34536261
 KEYWORDS oligo cloning; fis (full insert sequence).
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

Matches 1657;	Conservative	0;	Mismatches	1;	Indels	1;	Gaps	1;
---------------	--------------	----	------------	----	--------	----	------	----

TITLE

Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Iisogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length

JOURNAL

Nat. Genet. 36 (1), 40-45 (2004)

REFERENCE

32

TITL

NEDO human cDNA sequencing project

REFERENCE

3 (bases 1 to 2838)

TITLE

Direct Submission

COMMENT

Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan key Technology Center etc.); 5' - & 3'-end one pass sequencing: RAB HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.

nos

1. .2838

8587.2838

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Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1657; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1.

QY	47	CAGGCACGACATCTCTTCAGAAAAAGCATCCCCGAGAGAGAAACGAAATCGTAAATCATCT	106
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QY	107	AGGTCAGCTGAGGCTCTCGGAAATTTGTCTCTTCAGTGGAAACCCGAGAAAGCTGATC	166
Db	1240	AGGTCAGCTGAGGCTCTCGGAAATTTGTCTCTTCAGTGGAAACCCGAGAAAGCTGATC	129
QY	167	AGTTCCTCAGTCTTAAACAAATGSCCCAGGGTTTGGTACGCTTGCAGCTGATG	226
Db	1300	AGTTCCTCAGTCTTAAACAAATGSCCCAGGGTTTGGTACGCTTGCAGCTGATG	135
QY	227	ACTTTTCCAGAGAGAGTGCGGCTGTCTGAACTGTGCTCAGAGGAGCTGTATCTGGAGC	286
Db	1360	ACTTTTCCAGAGAGAGTGCGGCTGTCTGAACTGTGCTCAGAGGAGCTGTATCTGGAGC	141
QY	287	TGATGCTGAGAACTACAGTAACCTTGTGCTCAGTGGATTTTGGAGTCAGCATATGAAATA	346
Db	1420	TGATGCTGAGAACTACAGTAACCTTGTGCTCAGTGGATTTTGGAGTCAGCATATGAAATA	147
QY	347	AGAGTTTACCTTACAG-AAAAAACATTTATGAAATTAAGGCTTCCAAAGAAATTCAGAT	405
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QY	406	AGAGAAGTAATCCCTTGCGCGCTTAACGTGATATGTGAAGGTACGCTTGAAAGACCAAG	465
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QY	466	CGCTTCAGAGGAGGTATGTCAATCAGATATCATCAATTATGTCAAAAGCCTGCTACT	525
Db	1600	CGCTTCAGAGGAGGTATGTCAATCAGATATCATCAATTATGTCAAAAGCCTGCTACT	165
QY	526	AGAGAAGGACCCCTCCTAGAAACATCAGAGACATCAATAAGAGAAATTCCTTTGAATGT	585
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QY	766	AAGGCTTTGCATGGGGGCTCAAGCCTCGTATATCAATAAGAGATTCATATCTGGTAAAAA	825
Db	1900	AAGGCTTTGCATGGGGGCTCAAGCCTCGTATATCAATAAGAGATTCATATCTGGTAAAAA	195
QY	826	CCCTATGATGTAAAGACTGTGAAAGGCTTTGCGGCTGTGTATGATGCTCAGCAGC	885
Db	1960	CCCTATGATGTAAAGACTGTGAAAGGCTTTGCGGCTGTGTATGATGCTCAGCAGC	201
QY	886	CAGAGATTTCCACTGCGGAGAAAGACTACGAATGCCAAAGACTGTGGGAAAGCTTTTAC	945
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QY	946	CGTGTGTAAACCTAATTCAGCAACAAGAAATTCATATGTGGGGAAGGCTTACAGAGTGT	1001
Db	2080	CGTGTGTAAACCTAATTCAGCAACAAGAAATTCATATGTGGGGAAGGCTTACAGAGTGT	213
QY	1006	AAAGACTGTGGAGGCTTTTATTTGTGTTCAGGCTTCATTCAGCATTAAGAAATTCAC	1061
Db	2140	AAAGACTGTGGAGGCTTTTATTTGTGTTCAGGCTTCATTCAGCATTAAGAAATTCAC	219

QY 1066 ACAGGTGGAACCTTATGAATGTCAGAAATGGGAAAGGCTTACTCTGAGTCAATTAC 1125
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 QY 1126 CTTACTCAGCATCAGAAATGTCACACCGGTGAGAAAGCTTCAGAAATGTAAGAGTGTGG 1185
 DB 2260 CTTACTCAGCATCAGAAATGTCACACCGGTGAGAAAGCTTCAGAAATGTAAGAGTGTGG 2319
 QY 1186 AAGGCTTTTCCGTGGGTTTCAGAGCTCTGTTAAGCAGAGAGATACATACGGGCGAAG 1245
 DB 2320 AAGGCTTTTCCGTGGGTTTCAGAGCTCTGTTAAGCAGAGAGATACATACGGGCGAAG 2379
 QY 1246 CCGTCAAGTGCACGAATGTGGGAAAGGCTTCATTTGTGCTATCACTCACTGACAC 1305
 DB 2380 CCGTCAAGTGCACGAATGTGGGAAAGGCTTCATTTGTGCTATCACTCACTGACAC 2439
 QY 1306 GAGAGATTCACACAGCGGAAACCCGTAATAATGTAAAGAGTGTGGAAAGGCTTCAAT 1365
 DB 2440 GAGAGATTCACACAGCGGAAACCCGTAATAATGTAAAGAGTGTGGAAAGGCTTCAAT 2499
 QY 1366 TATGATCGAGCTCTGTGAAACATGAGAAATTCATACCGGGGTGAAACCTATGGGTGT 1425
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 QY 1426 ACAGAAATGTGGAAAGCTTTAGTCAACCGCCATCACTTACACACATCAGAAACGAC 1485
 DB 2560 ACAGAAATGTGGAAAGCTTTAGTCAACCGCCATCACTTACACACATCAGAAACGAC 2619
 QY 1486 AGTGGGCGGAATTCCTACGAATGTAAAGAGTGTGGGAAAGGATGTAAACCACTTAACAT 1545
 DB 2620 AGTGGGCGGAATTCCTACGAATGTAAAGAGTGTGGGAAAGGATGTAAACCACTTAACAT 2679
 QY 1546 CTCCGAGAAATCAGAGATTCACAAACAGTTGAAAGGCTTTGAAACGAGTACGCCGT 1605
 DB 2680 CTCCGAGAAATCAGAGATTCACAAACAGTTGAAAGGCTTTGAAACGAGTACGCCGT 2739
 QY 1606 CGTATCTATGTTTGGCTTTCACAGTTTGTAACTCTGACAGTCACTGACGTTCAAAATA 1665
 DB 2740 CGTATCTATGTTTGGCTTTCACAGTTTGTAACTCTGACAGTCACTGACGTTCAAAATA 2799
 QY 1666 TTAATGGAATTCAGAAATTAAGAAATTTTAAGTCTC 1704
 DB 2800 TTAATGGAATTCAGAAATTAAGAAATTTTAAGTCTC 2838

RESULT 12
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 ACCESSION CS118206
 VERSION CS118206.1 GI:70666152
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 1. Bertucci, F., Houlgate, R., Birnbaum, D. and Debono, S.
 Gene expression profiling of colon cancer by dna microarrays and
 correlation with survival and histoclinical parameters
 Patent: WO 2005054508-A 253 16-JUN-2005;
 Ibisogen (FR); Institut Paoli-Calmettes, Ipc (FR); Institut National
 de la Sante et de la Recherche Medicale (INSERM) (FR)
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ORIGIN
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Query Match 80.4%; Score 1619.4; DB 6; Length 2196;
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 Matches 1660; Conservative 0; Mismatches 1; Indels 30; Gaps 1;

QY 47 CAGGCGACATCTTTCAGAAAAAGCATCCCGAGAGAGAAAGCAATGTTAAACATCTT 106
 DB 490 CAGGCGACATCTTTCAGAAAAAGCATCCCGAGAGAGAAAGCAATGTTAAACATCTT 549
 QY 107 AGGTC-----AGCTTAAAGCTTCGGAAATTTGCT 136
 DB 550 AGGTCAGCTTTTACAGTGAAGAAACCGACACTGTGAGCTTAAAGCTTCGGAAATTTGCT 609
 QY 137 TCTTCAGTGAACCCCGAGAAAGTGAATGATCTTCACTTCTTAAACAAATGGCCAG 196
 DB 610 TCTTCAGTGAACCCCGAGAAAGTGAATGATCTTCACTTCTTAAACAAATGGCCAG 669
 QY 197 GTTTGTGACGTTCCGACGTAAGCATGACCTTTCTCAGAGAGAGTGGGCTGTG 256
 DB 670 GTTTGTGACGTTCCGACGTAAGCATGACCTTTCTCAGAGAGAGTGGGCTGTG 729
 QY 257 ACTGTCTCAGAGGAGCTGTATCTGGACGTGATGCTGAGAAATCTACATCTTGTCT 316
 DB 720 ACTGTCTCAGAGGAGCTGTATCTGGACGTGATGCTGAGAAATCTACATCTTGTCT 789
 QY 317 CACTGGAATTTGGAAGTCACTATGAAATTAAGATTTTACTTACAGAAAAAAACATTCATG 376
 DB 790 CACTGGAATTTGGAAGTCACTATGAAATTAAGATTTTACTTACAGAAAAAAACATTCATG 849
 QY 377 AAATTAAGGCTTCCAAAAAGAAATTCAGATAGAAAGTAAATCCCTTGGCCGTAACTGGA 436
 DB 850 AAATTAAGGCTTCCAAAAAGAAATTCAGATAGAAAGTAAATCCCTTGGCCGTAACTGGA 909
 QY 437 TATGTGAAGTACCGTTTAAAGACCAACGCCCTCCAGAGGAGTATGTCAATCGATGA 496
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 QY 497 TCATCAATTAATGTCAAAGGCTGTACTAGAGAAAGGACCCCTCTGAAACACATCAGA 556
 DB 970 TCATCAATTAATGTCAAAGGCTGTACTAGAGAAAGGACCCCTCTGAAACACATCAGA 1029
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 DB 1270 TTCATTAAGAGATTCATCTGTTGAAAAACCTTATGAATGTAAAGACTGTGAAAGGCT 1329
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 DB 1330 TTTGGCGGTGTGATGAGTCACTGACACAGAGATTCACATCGGGAGAAAGACTACG 1389
 QY 917 AATGCAAAAGACTGTGGAGAAAGCTTTAGCCGTGTATTAATCTTACAGACAAAGAGA 976
 DB 1390 AATGCAAAAGACTGTGGAGAAAGCTTTAGCCGTGTATTAATCTTACAGACAAAGAGA 1449
 QY 977 TTTCAATGTGGGAGAAAGCTTTACAGATGTAAAGACTGTGGAGAGGCTTTTATTTGTGTT 1036
 DB 1450 TTTCAATGTGGGAGAAAGCTTTACAGATGTAAAGACTGTGGAGAGGCTTTTATTTGTGTT 1509
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ORIGIN

Query Match 80.4%; Score 1619.4; DB 8; Length 2196;
 Beest Local Similarity 98.2%; Pred. No. 0;
 Matches 1660; Conservative 0; Mismatches 1; Indels 30; Gaps 1;

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 107 AGGTC-----AGCTTAGCCTCTCGAATTTGCT 136
 550 AGGTGAGCTTTACAGTAGAGAGAAACGACACTGTAGCTCTAGCCTCTCGAATTTGCT 609
 137 TCTTCAAGTGGAAACCCCGAGAGAGAGATGATCACTTCTTCAAGTGGAAACCCCGAG 196
 610 TCTTCAAGTGGAAACCCCGAGAGAGAGATGATCACTTCTTCAAGTGGAAACCCCGAG 669
 197 GTTGTGAGCTTTCGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 256
 670 GTTGTGAGCTTTCGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
 257 ACTGTGCTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
 730 ACTGTGCTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789
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 790 CACTGATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849
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 1390 AATGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1449
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 2110 TACCTGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2169
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 2170 TAACTCTCAA 2180

DB 2170 TAACTCTCAA 2180

RESULT 14
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 ACCESSION AC146884
 VERSION AC146884.3 GI:68268082
 KEYWORDS HTG;
 SOURCE Callithrix jacchus (white-tufted-ear marmoset)
 ORGANISM Callithrix jacchus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
 Callitrichidae; Callithrix.
 1 (bases 1 to 21932)
 Antoneilias,A., Ayele,K., Bass,D., Benjamin,B., Bera,J.,
 Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brookes,S., Chu,G.,
 Coleman,H., Engle,J., Fukukenko,T., Gestole,M., Greene,A., Guan,X.,
 Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P.,
 Hunter,G., Hurle,B., Idol,J.R., Kwong,P., Laric,P., Larson,S.,
 Lee-Lin,S.-O., Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B.,
 Margulies,E.H., Masello,C., Maskeri,B., McDowell,J., Mojidi,H.A.,
 Mullikin,J.C., Ostreicher,J.S., Park,M., Portnoy,M.E., Praead,A.,
 Puri,O., Reddix-Dugue,N., Sante,A., Schandler,K., Schueler,M.G.,
 Sison,C., Stantirpop,S., Stephen,E., Tave,A., Thomas,J.W.,

TITLE	Thomas,P.J., Tsipouri,V., Ung,L., Vogt,J.L., Weeberby,K.D.,
JOURNAL	Walters,T.R., Young,A. and Green,E.D.
REFERENCE	NISC Comparative Sequencing Initiative
AUTHORS	Unpublished
TITLE	2 (bases 1 to 219392)
JOURNAL	Green,E.D.
REFERENCE	Direct Submission
AUTHORS	Submitted (16-OCT-2003) NIH Intramural Sequencing Center, 8717
TITLE	Govemont Circle, Gaithersburg, MD 20877, USA
JOURNAL	3 (bases 1 to 219392)
REFERENCE	Green,E.D.
AUTHORS	Direct Submission
TITLE	Submitted (13-FEB-2004) NIH Intramural Sequencing Center, 8717
JOURNAL	Govemont Circle, Gaithersburg, MD 20877, USA
REFERENCE	4 (bases 1 to 219392)
AUTHORS	Green,E.D.
TITLE	Direct Submission
JOURNAL	Submitted (28-JUN-2005) NIH Intramural Sequencing Center, 5625
REFERENCE	Fishers Lane, Rockville, MD 20852, USA
AUTHORS	On Jun 26, 2005 this sequence version replaced gi:42544004.
TITLE	
JOURNAL	
COMMENT	

This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features section.

FEATURES

Location/Qualifiers

[illegible]

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ORIGIN

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Best Local Similarity	88.2%	Pred. No. 0;		
Matches 1674;	Conservative	0;	Mismatches 199;	Indels 25; Gaps 6;

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QY	172	TTCAATTCTAAAAACAATGATGCCAGGGTTGGTGAAGTTTCGCCAGCGTAGCCATTAGACTTT	231
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QY	532	GGCACCCCTCTTAGAACACATCAGAGACATCTAAAGAGAAATTCCTTTGAATGTAAAGAC	591
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DEFINITION Sequence 4050 from Patent WO02068579.
ACCESSION CQ718116
VERSION CQ718116.1 GI:42278973
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
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Patent: WO 02068579-A 4050 06-SEP-2002;
PB Corporation (NY) (US)
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OY 174 CAGTTCTAAACAAATGAGCCAGAGGTTTGTGACGTTCCGCGACGTAGCATAGACTTTTC 233
DB 61 CAGTTCTAAACAAATGAGCCAGAGGTTTGTGACGTTCCGCGACGTAGCATAGACTTTTC 120
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